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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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1: gb_ba1:
2: gb_ba2:
US-09-477-392-1
2954
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Gapop 10.0 , Gapext 1.0
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Copyright (c) 1993 - 2000 Compugen Ltd.
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gb_ba2:*
gb_om:*
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45: em_htg2:*

46: em_bum5:*

47: gb_htg8:*

49: gb_htg9:*

50: gb_htg11:*

51: gb_htg11:*

53: gb_htg12:*

54: gb_htg13:*

55: gb_htg13:*

56: gb_htg15:*

60: em_htg47:*

61: em_htg5:*

62: em_htg6:*

63: em_htg7:*

64: gb_htg18:*

65: gb_htg18:*

67: gb_htg18:*

68: gb_htg18:*

70: gb_htg18:*

71: gb_htg19:*

72: gb_htg18:*

73: gb_htg18:*

74: em_htg92:*

75: em_htg92:*

76: em_htg92:*

77: gb_htg18:*

78: gb_htg19:*

79: gb_htg23:*

71: gb_pt1:*

71: gb_pt1:*

72: gb_pt1:*

73: gb_pt1:*

74: em_htg9:*

75: em_htg9:*

76: em_htg9:*

77: gb_pt1:*

78: gb_pt1:*

79: gb_pt2:*

80: gb_gt2:*

81: gb_pp1:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

18 19 20 21	c 16	13 14 15	c 12	c 10	c 7	<b>சு</b> பெ்	c - 3 2 F	Result No.
279.4 278.4 278.4 278.4 278.4	282.8 281	304.6 299.8 283.6	315.2 310.4	315.8	719 315.8	1256.4	2954 2729 2719.4	Score
999.5	9.51	10.3 10.1 1 9.6 2	10.7 10.5 1	10.7 1	24.3	42.5 1	100.0 92.4 1 92.1	Query Match Length DB
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78 78 79	55	11 39 65	37 9	77	78 8	58 40	37 37	BB
HSG5 HSZNE74A3 HSZNE741 G27154	AC004877 AC060772	MMZFP29 AC012313 AC079575	AK023017 AC007228	AC013570 HSAJ03147	HSM802596 AB002324	AC073111 AC015887	AF201303 AC005586 AK025356	ID
x82192 H.sapiens E AF072567 Homo sapi x71023 H.sapiens z G27154 SHGC-31580	AC004877 Homo sapi AC060772 Mus muscu	X55126 M.musculus AC012313 Homo sapi AC079575 Mus muscu	AK023017 Homo sapi AC007228 Homo sapi	ACO13570 Homo sapi AJ003147 Homo sapi	AL162065 Homo sapi AB002324 Human mRN	AC073111 Homo sapi AC015887 Mus muscu	AF201303 Homo sapi AC005586 Homo sapi AK025356 Homo sapi	Description

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REFERENCE
AUTHORS
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SOURCE
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Direct Submission
Submitted (02-NOV-1999) Pathology,
Medical Alumni Building, Burlington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The dhfr oribeta-binding protein RIP60 contains 15 z. DNA binding and looping by the central three fingers associated proline-rich region Nucleic Acids Res. 28 (2), 570-581 (2000) 10606657
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Mammalia; Eutheria; Primates
1 (bases 1 to 2954)
Houchens, C.R., Montigny, W.,
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chens,C.R., Gilbert,J.M. and
/product="dhfr oribeta-binding protein RIP60"
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/protein_id="AP26712.1"
/db_xref="g1:6716714"
/db_xref="g1:6716714"
/db_xref="g1:6716714"
/db_xref="d1:6716714"
/db_xref="d1:
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/db_xref="taxon:9606"
/cell_line="HeLa"
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5 AC079506
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AB046644
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AF16186 Homo sapi

AF16186 Homo sapi

AC016630 Homo sapi

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    CACACGGGCGAGCGCCCCACCAGTGCCCCGAGTGCGGGAAGCGCTTTACCAATAAGCCC
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RESULT AF201303 LOCUS

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FEATURES

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gtgcacgtagctgaggccctggaggaggccgcaggccaaggctctggggccccggcccagg
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                                                                                                                              ggccgccccgcggtgaccgccccgggcccggtggagatgccgtcgaccgccccttccag
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                                                              tgtgcctgttgttggcaagcgcttccggcacaagcccaacttgatcgctcaccgccgcgtg
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                                                                                                                                                                            GTGCACGTAGCTGAGGCCCTGGAGGAGGCCGCAGCCAAGGCTCTGGGGCCCCGGCCCAGG
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                                                 TGTGCCTGTTGTGGCAAGCGCTTCCGGCACAAGCCCAACTTGATCGCTCACCGCCGCGTG
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54; Conservative
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2040	ggccctgctagcgagagagtcaaccccggtggccagggaacccacttccaagcgcaggg	1981 1981	p Qy
1980 1980	tggagtaggggacaatgggaatcctagaggggatggaagatgcgggggagtgagctgggtg 	1921 1921	pb 99
1920 1920	gagagggctggggtccttcgtggtgggagtcgcagtgggctgggggtgcctgcc	1861 1861	g 49
1860 1860	ctcctggcccaccagaagaagcacgatgtctgagacggtgggcgggggccgtgttggctga 	1801	B 8
1800 1800	atcegggacggcgcttctgctgttgccatctgtggccagaccttcgacgacgaggagaga 		В 8
1740 1740	cccgactgcgaccgcagcttcagccagaagtccaacctcatcacccacc	1681 1681	DЬ
1680 1680	cagaagtccaacctggtgtcgcaccggcgcatccacacgggcgagcggccctacgcctgt 	1621 1621	음 2
1620 1620	cggcgcatccacaccggcgagaagccctacgtctgccccgactgcggcaaagccttcagc	1561 1561	B 8
1560 1560	cccttcgtgtgtcccgactgcggcaaggccttccgccacaaaccctacctggcgcggcac	1501 1501	B 6
1500 1500	cgccgcttctcccagggcagccatctggcggcgcatcggccggaccacgccccgatcgg	1441 1441	Db Qy
1440 1440	ctggtggcgcactcgccggtgcactccggcgagcggcccttcgcctgcgaggagtgcgcclll	1381 1381	B 8
1380 1380	accggggagcggccttcacctgcgccgagtgcggggaagaacttcggcaagaagacgcac 	$\omega$ $\omega$	Dy Qy
1320 1320	gacgactgeggcaggagctteeggetggagegetteetgegggeceaceageggeaegae	1261 1261	₽ \$
1260 1260	9999ccccgccagagcacccgcaggacccgatcgaagccccccctccct	1201 1201	\$ 5
1200 1200	gagtccgcggccgagcccaccccggcggtacctctgaaaccggcccaggagccgccca	1141 1141	Db Qy
1140 1140	9999991c999ccca99cc9ccco999ccc999gagccccagctgccagccggcccccag	1081	ОУ
1080 1080	ggccgccgcttccggcacaaacccaacctgctgtctcacagcaagattcacaagcgatcc 	1021	B 8
1020 1020	tatotgaottogcacoggogoatocacacoggogagaagcoctacocgtgcaaagagtgc 	961 961	gg Qy

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		.aaaaaaaa	Qy
	2940		Db
	2940	ccctccttttcaaactagagaataaacatttggttttagaaaaaaaa	Оу
	2880	2821 TATAATTTCTACCTATTGGGCCTTGTTCTGTTCTCTGGAACTAAACAGAACAATCATTA	Db
	2880	ataatttctacctattgggccttgttctgttctctggaactaaacagaacaaccattt	Qy
	2820	GTTAGAAATTCTAATTGTTAGAAATCCTTCCTTATAATGAATG	Db
	2820	attgttagaaattctaattgttagaaatccttccttataatgaatg	Qy
	2760	2701 CTCTGCTTGAGCACTTAGGTGACAGGAACCTTCCGCACCTCCTGAGGCCCCTGGATGATTCT	da .
	2760		Qy
	2700	GCTGAGGGGAAGTTGCTGGTGAGTTTCCTTTCTCCATTTCTAGCATATGACACCTGG	Db
	2700	agctgaggggaagttgctggtgagtttcctttctccatttctagcatatgacacctg	Qy
	2640	2581 TTCGCTCCTTCCACAGCTCAGCATGTCACGGCAAGGACTGCCGCATTGGTGATGGAGGGC	Db
	2640	togotoottocacagotoagoatgtoacggoaaggactgcogoattggtgatggaggg	Qy
	2580	2521 CCTCCCCTGGCTGTCAGCAGCACTGTGTCCAGGCTCTTGTCTGAACACCCGCAGCCCCTCC	Db
	2580	ctcccctggctgtcagcagcactgtgtccaggctcttgtctgaacacccgcagcccctc	Qγ
***	2520	2461 CCAAGGCATTTACTCCTTGGTCTGTCTCGCTTTATCTGTCGCCCCCTCCCAGCGCTGAGAG	Db
•••••	2520	caaggcatttactccttggtctgtctcgctttatctgtcgcccctcccagcgctgaga	Ωу
	2460	2401 ACTTGGAGAGACCCGTCTGCTGTTAATACTTCCATCCTCCTTCCCCAAAGAGAGCAGATC	Db
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-	2400	2341 AAGCGAAGCCACTCTTACCTCTCCCTTCCCCTCCCACCTGCCCCCTGCGTAGGCACCCAG	Db
	2400	cgaagccactcttacctctcccttcccctcccacctgcccctgcgtaggcacc	Qy
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_	2340	ttggagaacctgctggccttgttagacagaacttgggcctttgccagcagcaagaggt	Οу
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	2280	catttttggaagcaggcgtggtagagtcctgtaaatgaatg	Qy
	2220	2161 GCCCTCCATCCTCTGGTATTAACGCCTTAATGCCCCTGTCTTTTACTGTAAGTTACTTAG	Db
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	2100	2041 ACGCCGGCCTCCAGCTGGTGTGCTAAGGCTCCGTCCTGACTGCCCTGTGCCCTGGAAA	뮹
	2100	gccggcctccagctggtgtgtgctaaggctccgtcctgactgccctgtgccctggaa	Qy

RESULT 2
AC005586/c
LOCUS
LOCUS
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AC005586 132150 bp DNA
DEFINITION Homo sapiens PAC clone RP4-584D14 from 7q31-q35, complete sequence.
ACC05586
VERSION
AC005586
VERSION
AC005586.2 GI:8468933
KEYWORDS
HTG.
SOURCE human.

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REFERENCE
AUTHORS
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                                                                                                                                                                                                                                                            University Genome Sequencing Center. For additional information about the map position of this sequence, see http://www.nhgri.nih.gov/DIR/GTB/CHR7, send mailto:egreen@nhgri.nih.gov, or see http://genome.wustl.edu/gsc
                                                                                                                                                                                                                                                                                                                                                 The sequence of this clone was established as part of a mapping and sequencing collaboration between the NHGRI Chromosome 7 Mapping Project (Eric D. Green, Director), John D. McPherson in the Department of Genetics (Washington University), and the Washington University Genome Sequencing Center. For additional information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
Submitted (30-SEP-2000) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 6
On Jun 12, 2000 this sequence version replaced gi:3907529.
                                                                                                        This clone was derived from human PAC library RPCI-4, prepared by Pieter de Jong and coworkers at the Roswell Park Cancer Institute (http://bacpac.med.buffalo.edu) using the method described by Ioannou et al., Nature Genetics 6:84-9 (1994). The library is from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Waterston, R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (12-JUN-2000) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Waterston, R.H.
Direct Submission
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Submitted (01-SEP-1998) Genome
University School of Medicine,
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The sequence of Homo sapiens
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Sulston, J.E. and Waterston, R.
                                                        The clone may be obtained either from Genome Systems,
                                                                                    one male donor
                                                                                                                                                                                                                           SOURCE INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MAPPING INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   restriction digest.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This sequence was finished as follows unless otherwise noted:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MO 63108,
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(http://www.genomesystems.com) or Research
(http://www.resgen.com); or from Pieter de
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (bases 1 to 132150)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Web site: http://genome.wustl.edu/gsc
Contact: sapiens@watson.wustl.edu
------ Summary Statistics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Center: Washington University Genome Sequencing Center Center code: WUGSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   neighboring data submissions.
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Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              to 132150)
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  de Jong
                            Genetics,
                            Inc.
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                                                                                                             is from
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NEIGHBORING SEQUENCE INFORMATION:

misc\_feature misc\_feature

/note="similar to

.8451

/note="match to EST AA129215 (NID:g1689084) zn84b02.s1"

EST AW246540 (NID:g6589533)"

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FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The clone sequenced to the right is RP5-820A21, 200 base pair overlap. Actual start of this clone is at base position 1 of RP4-584D14; actual end is at base position 131954 of RP4-584D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          represented by sequence derived by PCR from genomic DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /rpt_famil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /rpt_family="MIR" 4037. .4199
                                                                         7886.
                                                                                                                                                                                                                                                          /rpt_family="MER4-group" 6695 7007
                                                                                                                                                                                                                                                                                                /rpt_family="Alu" 6453. .6690
                                                                                                                                                                                                                                                                                                                                                                      /rpt_family="MIR" 5947. .5952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /rpt_family="L2"
1733. .2080
/note="similar to
7886. .8403
                                                                                                            /note="match to EST AI144211 (NID:g3666020) gb93g11.x1" 7883. .8397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /rpt_famil 3795. .388
                                    /note="match to EST 7886. .8562
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/clone="RP4-584D14"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                    /note="match to EST AA482420 (NID:g2210098) zt34f02.r1"
5148. .6450
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                                                                                         note="match to EST W72943 (NID:g1383235) zd54f12.r1"
                                                                                                                                                                                     7180
                                                                                                                                                                                                     rpt_family="MER4-group"
                                                                                                                                                                                                                                                                                                                                                                                                                                                             'note="similar to
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                                                      AI144211 (NID:g3666020) qb93g11.x1"
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                  (NID:g6936822) fhlld05.yl"
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Best Local Similarity 99.1
Matches 2796; Conservative
                                                                                                                                                                                                                                                             347 ggcttcacacccgccggtgccaggcccggctgcccttgccctgccctgagtgtggccgtc 406
                                                                10646 GCCTGGCCCAGCCCCGACTCCTTTCTGGGCCCTCCCAGGAGTCACCCCAGACCCCTGGGGA 10587
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                                                                                                                                                  aggagtcccgcgggctgaggcaacaaggcacgtcagtggcccagtctggtgcccaagccc
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/note="match to EST AA059375 (NID:g1553199) zf66g07.rl"

8433. 8746
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/note="match to EST R72488 (NID:g846520) yj90g06.rl"
7976. .8575
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/note="similar to Oryctolagus cuniculus EST C83534
(NID:93062491)"
8841. 9377
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8707. .8845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="match to EST 8776. .9343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="match to EST AA053336 (NID:g1543923) zf60d12.r1"
8591. 9167
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            'note="similar to
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'note="similar to EST AA843440 (NID:g2929958) ak07h10.s1"
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ote="simil
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99.1%;
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                                                                                                                                                                                                                                                                                                                           Score 2729; Di
Pred. No. 0;
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1546	${\tt acgcccccgatcggcccttcgtgtgtccccgactgcggcaaggccttccgccacaaaccct}$	1487	у
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1426	caagaagacgcacctggtggcgcactcgccggtgcactccggcgagcggcccttcgcc	1367	Qy
9447	ACCAGCGGCAGCACACCGGGGAGCGGCCCTTCACCTGCGCCGAGTGCGGGAAAAACTTCG	. 9506	망
1366	ccagoggcacgacaccgggggagcggcccttcacctgcgccgagtgcgggaagaacttc	1307	Qy
9507	CTACAGCTGCGACGACTGCGGCAGGAGCTTCCGGCTGGAGCGCT	9566	Дb
1306	cctctacagctgcgacgactgcggcaggagcttccggctggagcgcttcctgcgggcc	1247	Qу
9567	AGGAGCCGCCAGGGGCCCCCCAGAGCACCCGCAGGACCCGATCGAAGCCCCCCCT	9626	рb
1246	gaagcogcogatogaaggcoccogccagagcaccogcaggaccogatcgaagccccccc	1187	Qγ
9627	CAGCCGGCCCCAGGAGTCCGCGGCCGAGCCCACCCCGGCGGTACCTCTGAAACCGGCCC	9686	Дb
1186	agccggcccccaggagtccgcgggccgagccacccggcggtacctctgaaaccggcc	1127	Qy
9687	TCACAAGC	9746	Ъ
1126	acaagcgatccgaggggtcggcccaggccgccccggcccggggagcccccagctg	1067	Qy
9747	CGTGCAAAGAGTGCGGCCGCCGCTTCCGGCACAAACCCAACCTGCTGTCTCACAGCAAGA	9806	뫄
1066	gtgcaaagagtgcggccgccttccggcacaaaccccaacctgctgtctcacagcaaga	1007	Qy
9807	TTACCAATAAGCCCTATCTGACTTCGCACCGGCGCATCCACACCGGCGAGAAGCCCTACC	9866	Db
1006	taccaataagccctatctgacttcgcaccggcgcatccacaccggcgagaagccctac	947	Qy
9867	CTCACCGCCGCGTGCACACGGGGCGAGCGGCCCCACCAGCTGCCCGAGTGCGGGAAGCGCT	9926	Дb
946	tcaccaccagicgicacacaggicgagicgiccaccagitgicccgagitgicgigaagicgi	887	Qy
9927	ACCGCCCCTTCCAGTGTGCCTGTTGTGGCAAGCGCTTCCGGCACAAGCCCAACTTGATCG	9986	ДD
886	ccgcccttccagtgtgcctgttgtggcaagcgcttccggcacaagcccaacttgatc	827	Qy
9987	GGCCCCGGGCCCAGGGGCCCCCCCGCGGTGACCCCCCCCGGCCCGGTGGAGATGCCGTCG	10046	Дb
826	geceggeceggeggeggeggeggeggegeeggeeggegggggg	767	Qy
10047	TTGCCCACAAGCGGGTGCACGTAGCTGAGGCCCTGGAGGCGCGCAGCCAAGGCTCTGG	10106	Дb
766	tycccacaaycyyytycacytayctyayycctygayyayyayycycayccaayyctcty	707	οу
10107	AGGCCCGGCCTTCATATGCGGCAACTGTGGCCGGAGCTTTGCCCAGTGGGACCAGCTAG	10166	Db
706	ggcccggcccttcatatgcggcaactgtggccggagctttgcccagtgggaccagcta	647	Qy
10167	GCTTCTGGCGACGAAAGCAGCTTCGAGCTCATCTGCGGCGGTGCCACCCTCCCGCCCCGG	10226	Db
646	rttctggcgacgaaagcagcttcgagctcatctgcggcggtgccaccctcccgccccg	587	Qу
10227	TGCATCTGCGGGCCCATTCAGCTGCAAAGCGGCCCATCGCTTGTCCCAAATGCGAGAGAC	10286	Db
586	gcatctgctggcccattcagctgcaaagcaacccatcgcttgtcccaaatgcgagaga	527	ν,
10287	ACCTGGGCTTTGCCTGCCACCTCTGTGGGCAGACCTTCCGAGGCTGGGTGGCCCTGGTTC	10346	Db
526	.cctgggctttgcctgccacctctgtgggcagagcttccgaggctgggtggccctggtt	467	Qγ
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                                                                                                                                                                                                                                                                                                          Submitted (29-AUG-2000) to the DDBJ/EMBL/GenBank databases. Sugano, Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure Analysis, Human Genome Center Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639, Japan (E-mail:cdnal@ims.u-tokyo.ac.jp, Tel:81-3-5449-5286, Fax:81-3-5449-5416)
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Sugano,S., Suzuki,Y., Ota,T., Obayashi,M.,
Shibahara,T., Tanaka,T. and Nakamura,Y.
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/clone="COLU09895"
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Dobner, T.G.
                                 Eukaryota; Metazoa; Chordata; Craniata; Eukaryota; Metazoa; Chordata; Craniata; Eutheria; Primates; Catarrhini; Hominida 1 (bases 1 to 2878) Dobner, F.G., Fischer, M. and Groitl, P. Cloning of a novel zinc finger protein Unpublished
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aggcccggcccttcatatgcggcaactgtggccggagctttgcccagtgggaccagctag
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                                                                                   tycatctyctgycccattcayctycaaagcaacccatcycttytcccaaatycyayac
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                                                                         TGCATCTGCGGGCCCATTCAGCTGCAAAGCGGCCCATCGCTTGTCCCAAATGCGAGAGAC
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L786 L729	1/4/ accycaagayccacatccygyacygcyccttctyctyttyccatctytygccagaccttcy 1	Db 167
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1246	187 aggagccgccgccaggggccccgccagagcacccgcaggacccgatcgaagcccccct 1 	Qy 118
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326 769	767 ggccccggcccaggggccgcccgcggtgaccgcccccggccccggtggagatgccgtcg 8 	Qy 71
766	707 ttgcccacaagcgggtgcacgtagctgaggccctggaggaggccgcagccaaggctctgg 7 	Qy 70
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Qy Qy	Qy Db	Qy Db	Q <b>y</b> Db	Qy Db	Qy Db	Qy Db	Qy Db	Qy	Qу	Qy Db	Qу	Qy	Qy Db	Qy	Qу	Qy Db
2740 2690 2800	2681 2630	2622 2570	2562 2510	2503 2450	2444 2390	238 <b>4</b> 2330	2324 2270	226 <b>4</b> 2210	220 <b>4</b> 2150	2145 2090	2086 2030	2027 1970	1967 1910	1907 1850	1847 1790	1787 1730
octgaggcctggatgattctaattgttagaaattctaattgttagaaatccttcct	totagcatat-gacacotggcototgottgagcacottaggtgacaggaacottcogcacot 	cgcattggtgatggagggccagctgaggggaagttgctggtgagtttcc-tttctccatt 	tgaacaccgcagcccctccttcgctccttccacagctcagcatgtcacggcaaggactgc 	ccctcccagcgctgagagcctcccctggctgtcagcagcactgtg-tccaggctcttgtc	ttcccaaagagcagatcccaaggcatttactcctt-ggtctgtctcgctttatctgtcgc 	cctgcgtaggcacccagacttggagagacccgtctgctgttaatacttccatcctttcc 	gccagcagcagaggtgaagcgaagccactcttacctctcccttcccctcccacctgccc 	ctctgggctagatacagcttggagaacctgctggccttgttagacagaacttgggccttt 	tactgtaagttacttagatcatttttggaagcaggcgtggtagagtcctgtaaatgaatg	caccagtggaaaggaag-ccctccatcctctggtattaacgccttaatgcccctgtcttt 	cctgtgccctggaaaagcagcaata-catccgccccttacagccctctggctagaggagc 	ttccaagcgcaggga-cgccggcctccagctggtgtgtgtgtctaaggctccgtcctgactgc	gagtgagctgggtgggccctgctagcgagagaggtcaaccccggtggccaggggaacccac 	tgcctgcctagtgctggagtaggggacaatgggaatcctagaggggatggaagatgcggg 	gccgtgttggctgagagagggctgggggtccttcgtggtgggagtcgcagtgggctggggg 	acgacgaggagagactcctggcccaccagaagaagcacgatgtctgagacggtgggcggg 
2799 2749 2859	2739 2689	2680 2629	2621 2569	2561 2509	2502 2449	2443 2389	2383 2329	2323 2269	2263 2209	2203 2149	2144 2089	2085 2029	2026 1969	1966 1909	1906 1849	1846 1789

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AUTHORS
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                                                                                                                                                                                                                                                    Sequencing vector: presented, of reads chemistry: Dye-primer ET; 100% of reads Chemistry: Dye-terminator Big Dye; 0% of reads Assembly program: Phrap; version 0.990319 Consensus quality: 160317 bases at least Q40 Consensus quality: 166937 bases at least Q30 Consensus quality: 169751 bases at least Q20 Insert size: 17900; agarose-fp Insert size: 17900; agarose-fp Quality coverage: 4.24 in Q20 bases; agarose-fp Quality coverage: 4.24 in Q20 bases; sum-of-contigs
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Direct Submission
Submitted (08-JUN-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St.
MO 63108, USA
On Jul 15, 2000 this sequence version replaced gi:8572520.
                                                                                                                                                                                                                                                                                                                                                                                   Sequencing vector: M13; 100%
Sequencing vector: plasmid; 0%
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Center: Washington
Center code: WUGSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The sequence of Homo sapiens clone Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 179225)
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Homo sapiens chromosome
31 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                      Center project name: H_NH0511P07
                                                                                                                                                                                                                                                                                                                                                                                                                                 Web site:http://genome.wustl.edu/gsc/index.shtml
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HTG; HTGS_PHASE1; HTGS_DRAFT
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                                                                                                                                                       runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                NOTE: This is a 'working draft' sequence. It currently consists of 31 contigs. The true order of the pieces is not known and their order in this sequence record is
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7 clone RP11-511P7, WORKING DRAFT SEQUENCE,
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                                                                                                                                                                                                                              /clone="RP11-511P7"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (17-NOV-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On May 30, 2000 this sequence version replaced gi:7249370. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       http://ftp.genome.washington.edu/RM/RepeatMasker.html
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HTG; HTGS_PHASE1; HTGS_DRAFT.
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                                                                                                                                                                                                        NOTE: This is a 'working draft' sequence. It currently consists of 20 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence.
                                                                                                                                               as soon as it is available and the be preserved.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequencing vector: M13; M77815; 44% of reads sequencing vector: Plasmid; n/a; %-0.f% of reads 55.555555555556Chemistry: Dye-primer amersham; 58 Chemistry: Dye-terminator Big Dye; 42% of reads Assembly program: Phrap; version 0.960731 Consensus quality: 195610 bases at least Q40 consensus quality: 197810 bases at least Q20 consensus quality: 197810 bases at least Q20
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Insert size: 199558; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
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1161 2600:
1 1060: contig of 1060 bp in length
1061 1160: gap of 100 bp
1161 2600: contig of 1440 bp in length
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* 20294 20393: gap of 100 bp

* 20294 20393: gap of 100 bp

* 20394 24037: contig of 3644 bp in length

* 24038 24137: gap of 100 bp

24138 30849: contig of 6712 bp in length

30850 30949: gap of 100 bp

30950 44871: contig of 13922 bp in length

44872 44971: gap of 100 bp

61255 61354: gap of 100 bp

61355 74139: contig of 12785 bp in length

61355 74139: contig of 24911 bp in length

99151 99250: gap of 100 bp

74240 99150: contig of 24911 bp in length

99251 129995: contig of 24911 bp in length
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13423 15194: contig of 1772 bp in length
15195 15294: gap of 100 bp
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5831: contig of 1673
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This clone (DKFZp762K135) is available at the RZPD in Berlin. Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de Further information about the clone and the sequencing project is avail
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Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKF2); Email s.wiemann@dkfz-heidelberg.de;
sequenced by GBF (National Research Centre for Biotechnology Ltd.,
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97349984
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lmates; Catarrhini; Hominidae; Homo.
(bases 1 to 6045)
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Kazusa DNA Research Institute, Gene Structure 1; 1532-3
18arazu, Chiba 292, Japan (E-mail:cdnainfo@kazusa.or.jp,
p://www.kazusa.or.jp, Tel:+81-438-52-3930,
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SNLVQHQRTHTGEKPYKCTECEKAFTQSTNLIKHQRSHTGEKPYKCGECRRAFYRSSD
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/db_xref="taxon:9606"
/clone="HG0579"
/clone_lib="pBluescriptII SK
                                                                                                                                                                                                                                                   /sex="male"
                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                  tissue_type="brain"
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Best Local Similarity
   1470
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      a
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g
   1072
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Conservative

0;

10.7%;

Score 315.8; DB 8 Pred. No. 1.1e-39; Mismatches 517;

8:

Length Indels

6045; 12;

Gaps

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693 gtgggaccagctagttgcccacaagcgggtgcacgtagctgaggccctggaggaggccgc gtgcgggaagaacttcggcaagaagacgcacctggtggcgccactcgccggtgcactccgg gcgcttcctgcgggcccaccagcggcaccgacaggggagcggcccttcacctgcgccga cgagaagccctacccgtgcaaagagtgcggccgccttccggcacaaaccccaacctgct ccctcccgcccggaggcccggcccttcatatgcggcaactgtggccggagctttgccca ggcgcatcggccggaccacgccccgatcggcccttcgtgtgtcccgactgcggcaaggc cgagcggcccttcgcctgcgaggagtgcggccgccgcttctcccagggcagccatctggc CTCCACCCTCATCAAGCACCAGCGGACTCACCTGCGCGAGGACCCGTTCAAGTGCCCAGT CACGCACACAGGCGAGAAGCCCTACGAGTGCCTAGAGTGCGGCAAGAGCTTCGGCCACAG gatogaagooccoccoccototacagotgogacgactgoggoaggagottocggotgga cctctgaaaccggcccaggagccgccgccaggggccccgccagagcaccc-gcaggaccc CTTCGGCCAGAACCACAACCTCCTCAAGCACCAGAAGATCCACGCGGGCGAGAAGCCATA gagcccccagctgccagccggccccaggagtccgcggccgagcccaccccg--gcggta gtctcacagcaagattcacaagcgatccgaggggtcggcccaggccgccccgggcccggg CGAGAAGCCCTACAAGTGCGGCGAGTGCCGCCGGGCTTTCTACCGCAGCTCGGACCTCAT GTGCGAGAAAGCCTTCACCCAGAGCACCAACCTCATCAAGCACCAGCGATCCCACACCGG CGAGTGCGGCAAGAGCTTCACGCAGAGCTCGCACCTGGTGCAGCACCAGCGCACGC---agccaaggctctggggccccggcccaggggccgccccgcggtgaccgccccccggccccgg CCGCCCGGCGGGGGGGAGAAGCCCTACATCTGCAACGAGTGCGGCAAGAGCTTCAGCCA CGAGCGGCCCTACAAGTGCCCAGAGTGCGGCAAGAGCTTCAGCGTCAGCTCCAACCTCAT CCGCTGCACCGAGTGCGGGAAGAGCTTCATCCAGAGCTCGGAGCTGACCCAGCACCAGCG CCAGCACCAGGCCACCCACACAGGCGAGAAACCCTACAAGTGCCCCGAGTGCGGGAAGCG ----ACACCGGCGAGAAGCCCTACAAGTGCCCCGACTGCGGCAAGTGCTTCAGCTGGAG tggagatgccgtcgaccgcccttccagtgtgcctgttgtggcaagcgcttccggcacaa GTGGTCCAAGCTGCGGCACCAGCGCATCCACACGGGAGAGCGGCCCAACACCTGCTC 1529 1409 1307 1349 1289 1170 1007 1052 1469 1247 1187 1229 1067 947 887 827 872 812 752 656 692 992 772

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ctgtggccagaccttcgacgacgaggagagactcctggcccaccagaagaagcacga 1826
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                                                                                                                                                                                                                                                                                                                         Submitted (13-NOV-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On May 25, 2000 this sequence version replaced gi:7654731. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                               Smit, A.F.A. & Green, F. (1220 1227)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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HTG; HTGS_PHASE1; HTGS_DRAFT.
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Center project name: L2523
Center clone name: 2_C_24
Center clone name: 2_C_24
Center clone name: 2_C_24
Center clone name: 2_C_24
Chemistry: Dye-terminator Big Dye; 100% of reads
                                                                                                                                       Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
------ Project Information
                                                                                                                                                                                                                                              Center: Whitehead Institute/ MIT Center
                                                                                                                                                                                                                           Center code: WIBR
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RP11-2C24,
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arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown This record will be updated with the finished sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 be preserved.
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29740 29839: gap of 100 bp
29840 33467: contig of 3628 bp in length
33468 33567: gap of 100 bp
33568 37139: contig of 3572 bp in length
7140 37239: gap of 100 bp
7240 41052: contig of 3813 bp in length
105 4152: gap of 100 bp
153 4152: gap of 100 bp
153 4152: gap of 100 bp
153 4152: gap of 100 bp
154 41554 contig of 3813 bp in length
155 41564: gap of 100 bp
157 41564: gap of 100 bp
158 4504: contig of 4352 bp in longth
159 4504: gap of 100 bp
150 45604: gap of 100 bp
150 45604: gap of 100 bp
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1009 1108: gap of 100 bp
11109 2471: contig of 1363 i
2472 2571: gap of 100 bp
2572 4482: contig of 1011 i
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8776 18875: gap of 100 bp
18776 21003: contig of 2128 bp in length
1004 21763: contig of 2128 bp in length
104 22763: contig of 1660 bp in length
164 22863: gap of 100 bp
16 25765: contig of 2802 bp in length
16 25765: contig of 2526 bp in length
17 28391: contig of 2526 bp in length
18 28391: gap of 100 bp
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Location/Qualifiers
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50123. .54849
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clone_end:SP6
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/db_xref="taxon:9606"
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Best Local Similarity
Matches 668; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              81676 CCGCCCGGCGGGGGGGAGAAGCCCCTACATCTGCAACGAGTGCGGCAAGAGCTTCAGCCA 81617
                                   80845 CAACCACCAGCGCATCCACCGCGGCGAGCGGCCCTACATCTGCGCCGACTGCGGCAAGAG
                                                                                                                                                                                                                                                     81025 CTCCACCCTCATCAAGCACCAGCGGACTCACCTGCGCGAGGACCCGTTCAAGTGCCCAGT
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                                                                                                                                                                                                                                                                                                                                                                                                                         1171 cctctgaaaccggcccaggagccgcccggccaggggccccgccagagcaccc-gcaggaccc 1229
1530 cttccgccacaaaccctacctggcgcggcaccggcgcatccacaccggcgagaagcccta 1589
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                                                                                                         CGAGCGGCCCTACAAGTGCCCAGAGTGCGGCAAGAGCTTCAGCGTCAGCTCCAACCTCAT 80846
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Pred. No. 4.8e-40;
0; Mismatches 517;
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CTTCATCATGAGCTCCACCCTATCCGCCACCACGCATCCACACCGGTGAGAAGCCCTA

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 239566)

Bernot, A., Heilig, R., Clepet, C., Smaoui, N., da Silva, C., Petit, J.L., Devaud, C., Chiannilkulchai, N., Fizames, C., Samson, D., Cruaud, C., Caloustian, C., Gyapay, G., Delpech, M. and Weissenbach, J. A transcriptional Map of the FMF region Genomics 50 (2), 147-160 (1998)

98317529
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (07-JAN-1998) GENOSCOPE - 2 rue Gaston Cremieux, EVRY BP191, ELocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AJ003147.1 GI:2808656
HUMNK4 gene; mareno gene;
gene; olfactory receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
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                                                                                                 Join(6759. .6775,9222. .9357,9467. .975

/gene="mmp20"

Join(6759. .6775,6776. .9221,9222. .935)

9467. .9758,9759. .15041,15042. .16530)

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zinc finger protein; znfmf gene.
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/replace="ac"
66755. .108346
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complement(26351.
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                                                                                                                                                                                                                                                                                                                                                                                  gene="znfmf"
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Best Local Similarity
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Sg gene STS

CDS gene CDS gene

VTIENDTPLEELSKYVDISIIALTRNRRTRRWYTCPLCGKQFNESSYLISHQRTHTGE KPYDCNHCGKSFNHKTNLNKHERIHTGEKPYSCSQCGKNFRQNSHRSRHEGIHIREKI FKCPECGKTFPKNEEFVLHLQSHEAERPYGCKKCGRRFGRLSNCTRHEKTHSACKTRK

	1792	1733 agagocacatoogggacggoottotgotgtgocatotgtggocagacottogacgacg	0у 1
	48599	658 ACGCCTGCGACACCTGCGGCCACCGTTTCCGCAATAGCTCCAACCTGGCCCGCC	Db 48
	1732	673 acgcctgtcccgactgcgaccgcagcttcagccagaagtccaacctaatcacccacc	Qy 1
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	913 49439	854 gcaagegetteeggeacaageecaacttgategeteacegeegegtgeacaegggegage	Qy Db 49
	853 49499	794 tgaccgcccccggcccggtggagai	Qy Db 49
ω ··	sq	ry Match 10.7%; Score 315.4; DB 77; Length 239566; t Local Similarity 58.5%; Pred. No. 5.2e-40; thes 616; Conservative 0; Mismatches 416; Indels 21; Ga	Quer Best Matc

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REFERENCE
AUTHORS
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ORIGIN
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JOURNAL
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                                                                                     agatgccgtcgaccgcccttccagtgtgcctgttgtggcaagcgcttccggcacaagcc
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   CGCGTTCATCTTACACCAGAGAATCCACACCGGGGAGAAGCCATTTGCGTGCCCCGAGTG
                    caacttgatcgctcaccgcgcgtgcacacgggcgagcgcccaccagtgccccgagtg 935
                                                            TGGAGGCCCCAAGAAGCCGTGGAAATGCGGGGACTGCGGGAAGGCCTTCAGCTACTGTTC
                                                                                                                      CAGCGCGCCTGGGGCGAGCCCGAAGGAGAGGCATCCTGACAGCCGCCAGCGGGAGAGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (23-AUG-2000) to the DDBJ/EMBL/GenBank databases. Takao Sibmitted (23-AUG-2000) to the DDBJ/EMBL/GenBank databases. Takao Isogai, Helix Research Institute, Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:genomics@hri.co.jp, Tel:81-438-52-3952)

NEDO human cDNA·sequencing project supported by Ministry of International Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology; cDNA library construction, 5'- & 3'-end one pass sequencing and clone selection: Helix Research Institute (supported by Japan Key Technology Center etc.) and Department of Virology, Institute of Medical Science,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NEDO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Saito, K., Yamamoto, J., Wakamatsu, A., Masuho, Y. and Kanehori, K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Isogai,T., Ota,T., Hayashi,K., Sugiyama,T., Otsuki,T., Suzuki
Nishikawa,T., Nagai,K., Sugano,S., Ishibashi,T., Fujimori,K.,
Tanai,H., Kimata,M., Watanabe,M., Hiraoka,S., Ishii,S., Kawai
Saito,K., Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagahari,K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                oligo capping; fis (full insert sequence). Homo sapiens teratocarcinoma cell_line:NT2 clone_lib:NT2RP2 clone:NT2RP2005496.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AK023017 2382 bp mRNA
Homo sapiens cDNA FLJ12955 fis,
similar to ZINC FINGER PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 (bases 1 to 2382)
Isogai, T. and Otsuki, T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              human cDNA sequencing
                                                                                                                                                                                                                                                                         a
                                                                                                                                                                                                                                                                      /clone_lib="NT2RP2"
/note="cloning vector: pME18SFL3-mRNA from NT2 neuronal precursor cells after 2-weeks retinoic acid (RA) induction."
1 789 c 656 g 450 t
                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                    ocation/Qualifiers
                                                                                                                                                                                             10.7%;
56.5%;
                                                                                                                                                                                  0;
                                                                                                                                                                                 Score 315.2; DB 3
Pred. No. 1.8e-39;
D; Mismatches 463
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1 135.
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                                                HTG
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ccacacgggcgagcggccctacgcctgtcccgactgcgaccgcagcttcagccagaagtc 1712
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Metazoa; Chordata; Craniata;

Vertebrata; Euteleostomi;

130067 bp s chromosome

DNA 19, BAC

37295

(CIT-B-21A4), complete

06-APR-1999

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JOURNAL REFERENCE
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complement(5700
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complement(9302..9497)
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GKKPYKCDVCHKSFRYGSSLTVHQRIHTGEKPYBCDVCRKAFSHHASLTQHQRVHSGEK
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6894. .82
                                                                                                                                                                                                                            complement(5799. .5866)
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5864. .5996
                                                                                                                                                                                                                                                                                                                                                                           /rpt_family="Aluy"
complement(4953...
                                                                       /rpt_family="MIR" complement(8977.
                                                                                                                                                                         /rpt_family="L1MA9"
complement(6099. .6
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ECKVCSKAFTQKAHLAQHQKTHTGEKPYECKECGKAFSQTTHLIQHQRVHTGEKPYKC
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CGKAFSHRQSLSVHQRIHSGKKPYECKECRKTFIQIGHLNQHKRVHTGERSYNYKKSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /map="19q13.4 between D19S891 and ZNF134"
/Clone_lib="CIT-B Cal Tech BAC library"
/note="LLNL Clone Name: BC37295"
complement(4...320)
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/protein_id="AAD23606.1"
/db_xref="GI:4567178"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/db_xref="taxon:9606"
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//note="predicted exon, program: grail2exons_human_1.3,
frame: 2, quality: good, score: 57.000"

complement(20721. .20768)

//note="predicted exon, program: grail2exons_human_1.3,
frame: 0, quality: excellent, score: 100.000"

complement(21509. .21720)

//rpt_family="MIR"
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/note="BLASTN similarity to G44255 (13. .186); match: 0.99,
/score: 1.3e-63; database searched: month.na; WIAF-3903-STS

Human Thudson SANGER Homo sapiens STS genomic, sequence
tagged site [Homo sapiens]"

complement(17491. .17766)

/rpt_family="Aludo"
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/rpt_family="MIR"
21897 ... 21996
                                                                                                                       CKECSKTFSQNAHLAQHQKIHTGEKPYECKECGKAFSQIAHLVQHQRVHTGEKPYECI
ECGKAFSDGSYLVQHQRLHSGKRPYECLECGKAFRQRASLICHQRCHTGEKPYECKEV
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                                                                                                                                                                                              /translation="MKSQEEVEVAGIKLCKAMSLGSVTFTDVAIDFSQDEWEWLNLAQ
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TGEKPFECTECGKAFSQNAHLVQHQRVHTGEKYYQCKQCNKAFSQSAHLAQHQRVHTG
EKYPECIECGKAFSDCSSLAHHRRIHTGEKPYVGCKAFKQNASLIRHRKYYHTGE
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KPPDCIDCGKAFTSDLGSSLAHHRRIHTGEKPYEDCNOVGKAFSHGSSLTVHQRIHTGEKPYE
YECNICEKAFSHRGSLTLHQRVHTGEKPYECKECGKAFRQSTHLAHHQRIHTGEKPYE
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complement/10172
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/rpt_family="(GGAA)n"
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/product="BC37295_1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /rpt_family="AluJo"
join(23186. .23245,27268. .27607,30057. .31456)
/note="Hypothetical ZNF-like human protein"
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22540. .22611
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complement/coccc
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complement(19623. .19)
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19599. .19622
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complement/1610;
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complement/16011
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/rpt_family="AluJb"
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complement/100"
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complement/1000"
                                                                                               AFRQSVHLAHHQRIHTGESSVILSSALPYHQVL"
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/db_xref="GI:4567179"
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Best Local Similarity 56.2

atches 603; Conservative
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                   tcacagcaagattcacaagcgatccgagggtcggcccaggcccaggccccggggag
                                                                                               gaagccctacccgtgcaaagagtgcggccgccgcttccggcacaaacccaacctgctgtc
                                                                                                                                                                                                                     AGCGTTCATCTTACACCAGAGAATCCACACCGGGGAGAAGCCATTTGCGTGCCCCGAGTG
                                                                                                                                                                                                                                                                                             TGGAGGCCCCAAGAAGCCGTGGAAATGCGGGGACTGCGGGAAGGCCTTCAGCTACTGTTC
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CCACTGGCGCACGCACGGGCGAGAAGCCGCACCGCTGCGCCGACTGCGGCAAGGCCTT
                                                                    GAAGCCCTACGCCTGCCACGAGTGCGGCAAGGCCTTCAGCCAGGGCTCGTACCTGGCGTC
                                                                                                                                              cgggaagcgctttaccaataagccctatctgacttcgcaccggcgcgtccacacccggcga
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/complement(33334. .33460)
/rpt_family="LINB6"
34364. .3446"
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complement(34541. .34568)
/rpt_family="AT_rich"
35434. .35813
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31406
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/rpt_family="AT_rich"
complement(28510. .28645)
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/rpt_family="(GAAAA)n"
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/rpt_family="MIR"
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24791..24811
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complement(32604. ...
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/rpt_family="(GAA)n"
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6. .31671
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Location/Qualifiers

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X55126.1
                           Denny,P. and Ashworth,A.
A zinc finger protein-encoding
phase of spermatogenesis
Gene 106 (2), 221-227 (1991)
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M.musculus Zfp-29
                                                                                       Chester Beatty Laboratories, 2 (bases 1 to 2094)
                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Vertebrata; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                   Submitted (03-NOV-1990) Denny
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/note="zinc fingers"
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TECGQKFSQSSALITHRRTHTGEKPYQCGECGKNFSRSSNLATHRRTHLVEKPYKCGL
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KGFSQRSQLVVHQRTHTGEKPYKCLMCGKSFSRGSILVMHQRAHLGDKPYRCPECGKG
FSWNSVLIHQRIHTGEKPYRCPECGKGFSNSSNFITHQRTHLKEKLY*
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/db_xref="GI:55471"
/db_xref="SWISS-PROT:007230"
/translation="MAAEVPAVSTPLSPLVQVPQEEDEQAEVTTWILEDDAWVQEAVL
CEDGPESEPFPQSAGKGSPQEEDAAEGPQGALVRFRELCRRWLRPEVHTKEQMLTVLP
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LNISGGEGGQQSDGDSDFERDCGSGGAQGHAPGEDPRVVPSEGREVGQLIGLQGTYLG
EKPYECPQCGKTFSRKSHLITHERTHTGEKYYKCDECGKSFSDGSNFSRHQTTHTGEK
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/db_xref="taxon:10000"
/dev_stage="adult male"
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Consensus quality: 175352 bases at least Q40

Consensus quality: 181475 bases at least Q20

Consensus quality: 182252 bases at least Q20

Estimated insert size: 194270; agarose-fp estimation

Estimated insert size: 194270; agarose-fp estimation

Quality coverage: 8.32 in Q20 bases; agarose-fp estimation

Quality coverage: 8.82 in Q20 bases; sum-of-contigs estimation

Quality coverage: 8.82 in Q20 bases; sum-of-contigs estimation.

* NOTE: This is a 'working draft' sequence. It currently

* consists of 9 contigs. Gaps between the contigs

* are represented as runs of N. The order of the pieces

* tablity of the pieces
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AC012313.5 GI:7711546
DTGS PHASE2; HTGS_DRAFT.
                                                                                                                                                                                                                                                            Project Information
Center Project Name: 835906, BC800930
Center clone name: CITB-E1_2619J13
                                                                                                                                                                                                                                                                                                                                                 Center: Joint Genome Institute
Center Code: JGI
Web site: http://www.jgi.doe.go
                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (23-OCT-1999) Production Sequencing Facility, DOE Jo Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, On May 6, 2000 this sequence version replaced gi:7690197.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 18325)
DOE Joint Genome Institute.
Sequencing of Human Chromosome 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
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DOE Joint Genome Institute.
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* NOTE: This is a 'working draft' sequence. It currently coverage: 8.3 in Q20 bases; agarose of the pieces
                                                                                                                                                                                                                                                                                                                                                                Submitted (02-SEP-2000) Production Sequencing Facility, Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA
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Mammalia; Eutheria; Rodenti
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DOE Joint Genome Institute.
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is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
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Search completed: February 22, 2001, 03:04:53 Job time: 14351 sec

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

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Sugano,S., Suzuki,Y., Ota,T., Obayashi,M., Nishi,T., Shibahara,T., Tanaka,T. and Nakamura,Y.
                                                                                                                                                                                                                                                             NEDO human cDNA sequencing project supported by Ministry of International Trade and Industry of Japan; CDNA full insert sequencing: Research Association for Biotechnology; cDNA library construction, 5'- & 3'-end one pass sequencing: Departent of Virology and Human Genome Center, Institute of Medical Science, Traditional Control Center Control Control Control Center Cente
                                                                                                                                                                                                                                                                                                                                                                                       Laboratory of Genome Structure Analysis, Human Genome (Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639, Japan (E-mail:cdnal@ims.u-tokyo.ac.jp, Tel:81-3-5449-5286, Fax:81-3-5449-5416)
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Submitted (29-AUG-2000) to the DDBJ/EMBL/GenBank databases. Sumio Sugano, Institute of Medical Science, University of Tokyo,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kawabata,A., Hikiji,T., Kobatake,N., Inagaki,H., Ikema,Y. Okamoto,S., Okitani,R., Ota,T., Suzuki,Y., Obayashi,M., N Shibahara,T., Tanaka,T., Nakamura,Y., Isogai,T. and Sugan
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Homo sapiens cDNA: FLJ21703 fis,
HSA24553 Homo sapiens mRNA for AK025356
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 (bases 1 to 2878)
Dobner, T.G., Fischer, M.
Cloning of a novel zinc
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AP4 gene; A
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AF201303
AF201303.1 G
Houchens,C.R., Gilbert,J.M. and Heintz,N.H.
Direct Submission
Submitted (O2-NOV-1999) Pathology, University of Vermont,
Medical Alumni Building, Burlington, VT 05405, USA
Location/Qualifiers
                                                                                          The dhfr oribeta-binding protein RIP60 contains 15 zinc fingers: DNA binding and looping by the central three fingers and an associated proline-rich region Nucleic Acids Res. 28 (2), 570-581 (2000)
                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates; 1 (bases 1 to 2954)
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CDRSFSQKSNLITHRKSHIRDGAFCCAICGQTFDDEERLLAHQKKHDV"
1973 c 839 g 538 t
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Eukaryota; Metazoa; Chordata; Cri
Mammalla; Eutherla; Primates; Cai
1 (bases 1 to 132150)
Sulston, J.E. and Waterston, R.
Toward a complete human genome so
Genome Res. 8 (11), 1097-1108 (1)
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/AQSGAQAPGRAHRCHGCMSTAMCHAPFRALL
HRQVHAAATDLGFACHLCGQSEFGWALLVLLAHSAKQPIACPKCGERFRHAPFLAL
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RAHLRCHPPAPEARPFICGNCGRSFAQWDQLVAHKRVHVAEALEEAAAKALGPRPRG
RPAVTAPRRGGDAVDRPFQCACGKRFRHKPNLLAHRRVHTGERPHQCPECGRRFTNK
PXLTSHRRIHTGEKPYPCKECGRRFRHKPNLLSHSKIHKRSEGSAQAADGPGSPQLPA
GPQESAAEFTPAVPLKPAQEPPFGAPPHBQDPIEAPPSLYSCDDCGRSFRLERFLRA
LQRHDTGERFTCAECGKNFGKKTHLVAHSPVHSGERPFACEBCGRRFSQGSHLAAHR
HQRHDTGERFTTCAECGKNFGKKTHLVAHSPVHSGERPFACEBCGRRFSQGSHLAAHR
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/db_xref="taxon:9606"
/cell_line="HeLa"
130..1833
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HTGERPYACPDCDRSFSQKSNLITHRKSHIRDGAFCCAICGQTFDDEERLLAHQKKHD
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/protein_id="AAF26712.1"
/db_xref="GI:6716714"
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                                                                        Submitted (30-SEP-2000) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, On Jun 12, 2000 this sequence version replaced g1:3907529.
                                                                                                                                                                                                                           Direct Submission
Submitted (12-JUN-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
                                                                                                                                                         Waterston, R.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 (bases 1 to 132150)
Stoneking,T., Ozersky,P., Wohldmann,P. and Le,T.
The sequence of Homo sapiens PAC clone RP4-584D14
                                                                                                                                                                                                                                                                                              Waterston, R.H.
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                                                                                                                                                                                                                                                                                                                                                    Submitted (01-SEP-1998) Genome University School of Medicine,
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Web site: http://genome.wustl.edu/gsc
Contact: sapiens@watson.wustl.edu
                                      Center: Washington University Genome Sequencing Center Center code: WUGSC
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Louis,

USA

NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions

Center project name: H\_DJ0584D14

·---- Summary Statistics

all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest. This sequence was finished as follows unless otherwise noted:

sequencing collaboration between the NHGRI Chromosome 7 Mapping Project (Eric D. Green, Director), John D. McPherson in the Department of Genetics (Washington University), and the Washington University Genome Sequencing Center. For additional information about the map position of this sequence, see http://www.nhgri.nih.gov/DIR/GTB/CHR7, send MAPPING INFORMATION:
The sequence of this clone was established as part of a mapping 7 http://www.nhgri.nih.gov/DIR/GTB/CHR7 , send mailto:egreen@nhgri.nih.gov , or see http://genome.wustl.edu/gsc and

# SOURCE INFORMATION:

This clone was derived from human PAC library RPCI-4, prepared by Pieter de Jong and coworkers at the Roswell Park Cancer Institute (http://bacpac.med.buffalo.edu) using the method described by Ioannou et al., Nature Genetics 6:84-9 (1994). The library is from is from

one male donor.

The clone may be obtained either from Genome Systems, (http://www.genomesystems.com) or Research Genetics, I (http://www.resgen.com); or from Pieter de Jong. Inc.

VECTOR: PCYPAC2
The clone sequenced to the right is RP5-820A21, 200 base pair
The clone sequenced to the right is RP5-820A21, 200 base pair
Overlap. Actual end is at base position 131954 of RP4-584D14.

The sequence RP4-584D14 from base position 21655 to 22775 is rich. This region was sized with PCR from genomic DNA and the hindili digest with band size 3643 real, and 3642 insilico. the GT The

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                                                                                                                                                 /note="similar to 7886. .8451
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                                                     note="similar to
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                                                     EST A1868891 (NID:g5542895) wc49f12.x1"
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                                                        GGGAGCCCCCAGCTGCCAGCCGGCCCCCAGGAGTCCGCGGCCGAGCCCACCCCCGGCGGTA
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/note="similar to

8835. .9229

/note="similar to C
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8228. .8362
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8302. .8928
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8289. .8732
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8754. .9069
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Mismatches 0;
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Baldwin, J., Barna, N., Beckerly, R., Boguslavkiy, L., Boukhgalter, B., Brown, A., Castle, A., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Domino, M., Donelan, L., Doyle, M., Ferreira, P., FitzHugh, W., Forrest, C., Funke, R., Gage, D., Galgan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Lehoczky, J., Lieu, C., Locke, K., Macdonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K., McLaughlin, J., Maddrim, J., McEwan, P., McGurk, A., McKernan, K., McLaughlin, J., Maddrim, J., Petterson, K., Pollara, V., Riley, R., Roy, A., Santos, R., Severy, P., Peterson, K., Pollara, V., Riley, R., Roy, A., Santos, R., Severy, P., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Tirrell, A., Vassiliev, H., Vo, A., Wheeler, J., Wu, X., Wyman, D., Ye, W. J., Zimmer, A. and Zody, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            On May 30, 2000 this sequence version replaced gi:7249370. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (17-NOV-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
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Birren, B., Linton, L.,
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Mammalia; Eutheria; Rodentia;
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Quality coverag.

NOTE: This is a 'working draft' sequence. It currently NOTE: This is a 'working draft' sequence of the pieces consists of 20 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Center project name: L742
Center clone name: 315_E_6
Center clone name: 315_E_6
Center clone name: 315_E_6
Sequencing vector: M13; M7815; 44% of reads
Sequencing vector: Plasmid; n/a; %-0.f%% of reads
55.55555555556Chemistry: Dye-primer-amersham; 58
Chemistry: Dye-terminator Big Dye; 42% of reads
Chemistry: Dye-terminator Big Dye; 42% of reads
Chemistry: Dye-terminator Big Dye; 42% of reads
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                                                                                                                                                                                                                                                                                                                            Assembly program: Phrap; version 0.960731 Consensus quality: 192611 bases at least Q40 Consensus quality: 196150 bases at least Q30 Consensus quality: 197810 bases at least Q20 Insert size: 182000; agarose-fp Insert size: 199558; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.
------ Project Information
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24037: contig of 3644 bp in length
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30849: contig of 6712 bp in length
30949: gap of 100 bp
44871: contig of 13922 bp in length
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10095: gap of 100 bp
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74139: contig of 12785 bp in
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18405: contig of 3111 bp in
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20293: contig of 1788 bp in
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13322: contig of 2703 bp in
22: gap of 100 bp
15194: contig of 1772 bp in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens mRNA; cDNA AL162065
                                                 Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERWANY; Email: clone@rzpd.de Further information about the clone and the sequencing project is available.
                                                                                                                                                              Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de; sequenced by GBF (National Research Centre for Biotechnology Ltd.,
                                 at http://www.mips.biochem.mpg.de/proj/cDNA/
                                                                                                             This clone (DKFZp762K135) is available at the RZPD in Berlin
                                                                                                                               German Genome Project
                                                                                                                                                  Braunschweig/Germany) within the
                                                                                                                                                                                                                                Martinsried, GERMANY
                                                                                                                                                                                                                                              Submitted (15-MAR-2000) MIPS, Am Klopferspitz 18a,
                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates; 1 (bases 1 to 759)
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                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
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Pred. No. 1.1e-34;
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/organism="Homo sapiens" /db\_xref="taxon:9606"

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               248 acagcaagattcacaagcgatccgagggtcggcccaggcccccgggcccg 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               199;
                                                                          Direct Submission
Submitted (21-DEC-1999) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 6: On Sep 19, 1948 the sequence version replaced gi:3213120.
                                                                                                                                                                   Submitted (19-SEP-1998) Department of University, 4444 Forest Park Avenue, 4 (bases 1 to 128361)
                                                                                                                                                                                                                                                                                              Submitted (12-JUN-1998) Genome University School of Medicine,
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Homo sapiens PAC clone RP4-751H13 from
                                                                                                                                                          Waterston, R.
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The sequence of Homo sapiens PAC clone RP4-751H13
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Leonard, S., Graves, T.
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                                                                                                                                                                                                                                                                                                                                                                                   Unpublished
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Web site: http://genome.wustl.edu/gsc
Contact: sapiens@watson.wustl.edu
                                  Center: Washington University Genome Center code: WUGSC
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/tissue_type="melanoma (MeWo cell line)"
a 246 c 252 g 144 t
                                                                                                                                                                                                                                                                                 USA
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67.9%;
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Pred. No. 4.3e-16;
0; Mismatches 94
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Center project name: H\_DJ0751H13

NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted: all regions were double stranded or sequenced with an alternate chemistry; an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:
The sequence of this clone was established as part of a mapping and sequencing collaboration between the NHGRI Chromosome 7 Mapping Project (Eric D. Green, Director), John D. McPherson in the Department of Genetics (Washington University), and the Washington Department of Genetics (Washington University), and the Washington University Genome Sequencing Center. For additional information about the map position of this sequence, see http://www.nhgri.nih.gov/DIR/GTB/CHR7, send mailto:egreen@nhgri.nih.gov or see http://genome.wustl.edu/gsc.meIGHBORING SEQUENCE INFORMATION: mapping and Mapping

The clone sequenced to the left is RP4-811N16, 200 bp overlap. Actual start of this clone is at base position 1 of RP4-751H13; actual end is at 128361 of RP4-751H13.

# Location/Qualifiers 1. .128361

FEATURES

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Submitted (05-NOV-1999) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. MO 63108, USA
On Jul 15, 2000 this sequence version replaced qi:8990985.
                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 210923)
Waterston, R.H.
                                                                                                                                                                                                             Direct Submission
                                                                                                                                                                                                                              2 (bases 1 to 210923) Waterston, R.H.
                                                                                                                                                                                                                                                                 Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                    AC013273.5 GI:9211421
HTG; HTGS_PHASE1; HTGS_DRAFT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens chromosome 10 unordered pieces.
                                                                                                                                                                                                                                                                                     The sequence of Homo sapiens clone
                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
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/rpt_family="MIR" 22848. .23146
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24983
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23773
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24894
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26933. .29260
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23679
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /rpt_family="Alu"
                                                                                                                              2000 this sequence version replaced gi:8990985
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                                                                                             -- Genome Center
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7 clone
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Summary Statistics

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BASE COUNT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Assembly program: Phrap; version 0.990319
Consensus quality: 200959 bases at least Q40
Consensus quality: 204292 bases at least Q30
Consensus quality: 206312 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chemistry: Dye-primer ET; 74% of reads Chemistry: Dye-terminator Big Dye; 26% of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequencing vector: M13; 74% Sequencing vector: plasmid; 26%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Insert size: 203000; agarose-fp
Insert size: 210023; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NOTE: This is a 'working draft' sequence. It currently consists of 10 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence {\bf r}
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104608
150644
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/db_xref="taxon:9606"
/chromosome="7"
                                                                                                              vector_side:left"
63763. .104507
                                                                                                                                               /note="assembly_name:Contig14
clone_end:SP6
                                                                                                                                                                              /note="assembly_name:Contigl3"
45801. .63662
                                                                                                                                                                                                                          vector_side:right"
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               /note="assembly_name:Contig17" 51422 c 51731 g 52663 t
                                                                                                                                                                                                                                                                                         /note="assembly_name:Contigl1"
                                                 /note="assembly_name:Contig16"
150744. .210923
                                                                                /note="assembly_name:Contig15"
104608. .150643
                                                                                                                                                                                                                                                           /note="assembly_name:Contigl2
                                                                                                                                                                                                                                                                                                               11908
                                                                                                                                                                                                                                                                                                                             /note="assembly_name:Contig10"
                                                                                                                                                                                                                                                                                                                                                                                            /note="assembly_name:Contig8"
                                                                                                                                                                                                                                                                                                                                                                                                                             /clone="RP11-428D5"
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45800: gap of
6362: contig
63762: gap of
104507: contig
104607: gap of
104607: gap of
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210923: contig
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of 7090
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unknown length
of 2088 bp in length
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REFERENCE
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DEFINITION
ACCESSION
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              M.musculus Zfp-29 gene for zz X55126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

[ bases 1 to 2094)
                                                                                                                                                                                                                                                                                                                                                                                                          phase of spermatogenesis
Gene 106 (2), 221-227 (1991)
                                                                                                                                                                                                                                                                                                                                                                                                                                        Denny,P. and Ashworth,A.
A zinc finger protein-encoding gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
Submitted (03-NOV-1990) Denny
Chester Beatty Laboratories, 2
2 (bases 1 to 2094)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Denny, P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           spermatogenesis; Zfp-29 gene; zinc-finger.
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                           /gene="Zfp-29"
/gene="Zfp-29"
/codon_start=1
/codon_start=1
/protein_id="CaA38920.1"
/protein_id="CaA38920.1"
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OEDGPESEPPOSAGKGSPOREDANGEPQGALVRFRELCRRWLRPEVHTKEOMLTVLP
REIQAWLQEHRPESSEEAVALVEDLTQTFRHSDFEIQSENGENSDEMFEGVESHGMF
LNISGGEGGGQOSDGSDFERDCGSGGAQGHAPGEDPRVVPSEGREVQQLIGLQGTYLG
LNISGGEGGGQOSDGSDFERDCGSGGAQGHAPGEDPRVVPSEGREVQQLIGLQGTYLG
EKPYECPQCGKTFSRKSHLITHERTHTGEKYYKCDECGKSFSDGSNFSRHQTTHTGEK
PYKCRDCGKSFSRSANLITHQRIHTGEKPFQCAECGKSFSRSPNLIAHQRTHTGEKPY
                                                                                                                                                                                                                                                                             /strain="ssp. domesticus"
/db_xref="taxon:1000"
/dev_stage="adult male"
                                                                                                                                                                                                             /gene="Zfp-29"
                                                                                                                                                                                                                                                /tissue_type="testis"
/clone_lib="Lambda ZAP cDNA"
                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                    organism="Mus musculus"
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DRGANISM
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Best Local Sim.
Matches 195;
                                                                                                                                                                                                                                             JOURNAL
                                                                                                                                                                                                                                                                                  AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 131 agcgctttaccaataagccctatctgacttcgcaccggcgcatccaccaccggcgagaaagc 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          71 tgatcgctcaccgcgcgtgcacacggggcggccgcaccagtgccccgagtgcggga 130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gcaagattcacaagcgatccgagggtcggcccaggccgccccggcccggggagccccc 310
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                          Center project name: H_NH0143I21
                                                                                                                                                                                  Submitted (14-JUN-2000) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. MO 63108, USA
On Jul 7, 2000 this sequence version replaced qi:8516162.
                 Sequencing vector: M13; 66%
                                                                                                             Center: Washington University Genome Center code: WUGSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE, 6 unordered pieces AC073314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens chromosome 7 c. SEQUENCE. 6 ......
                                                                                          Web site:http://genome.wustl.edu/gsc/index.shtml
                                                                                                                                                                                                                                                             Direct Submission
                                                                                                                                                                                                                                                                                  Waterston, R.H.
                                                                                                                                                                                                                                                                                                                  Unpublished
                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
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                                                                                                                                                                                                                                                                                                                                      The sequence of Homo sapiens
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/note="zinc fingers"
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KGFSQRSQLVVHQRTHTGEKPYKCLMCGKSFSRGSILVMHQRAHLGDKPYRCPECGKG
vector: plasmid; 34%
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Pred. No. 2.4e-13;
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                                                                                                                          Sequencing Center
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                                                                                                                                                                                                                                                                                     Local
                                                                                                            tgatcgctcaccgcgcgtgcacacgggcgagcggccccaccagtgccccgagtgcggga 130
AGAGCTTCATCCGCAAGCACCACCTCCTGGAACACCGGCGCATCCACACAGGCGAGCGGC 90059
                                      agogotttaccaataagooctatotgacttogcacoggogcatocacacoggogagaago 190
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Quality coverage: 7.94 in Q20 bases; agarose-fp Quality coverage: 8.07 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Insert size: 164000; agarose-fp
Insert size: 162070; sum-of-contigs
                                                                                                                                                                                                                                                                                     Similarity
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                                                                                                                                                                                                                                                                                                                                                                                               44044 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        be preserved.
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                                                                                                                                                                                                                                                                 Conservative
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96970. .162570
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4791. .12657
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="assembly_name:Contig16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="assembly_name:Contig13"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      note="assembly_name:Contig14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      note="assembly_name:Contig11"
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1462: gap of unknown length
4690: contig of 3228 bp in length
4790: gap of unknown length
12657: contig of 7867 bp in length
12757: gap of unknown length
14491: contig of 31734 bp in length
44591: gap of unknown length
96869: contig of 5278 bp in length
96869: contig of 52601 bp in length
162570: contig of 65601 bp in length
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Pred. No. 5.5e-14;
0; Mismatches 71
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                                                                           acttgatcgctcaccgcgcgtgcacacggggcgagcggccccaccagtgccccgagtgcg 127
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Prediction of the coding sequences of unidentified human genes. IX.

The complete sequences of 100 new cDNA clones from brain which can
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/protein_id="BAA25483.1"
/protein_id="BAA25483.1"
/db_xref="GI:3043638"
/tb_xref="GI:3043638"
/tb_xref="GI:3043688"
/tb_xref="
                                                                                                                                                                                                                                                                                                                                                                                                             DKPYTCPECGKGFSKTSHLTKHQRTHTGERPYKCLVCGKGFSDRSNFSTHQRVHTGEK PYPCPECGKRFSQSSSLVIHRRTHSGERPYACTQCGKRFNNSSHFSAHRRTHTGEKPY TCPACGRGFRRTDLHHHQRTHHGAGSLPTLQPVAPGGPGAKA"
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/clone_lib="pBluescriptII
/sex="male"
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/db_xref="taxon:9606"
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1. .1483
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Pred. No. 7.6e-13;
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                                               /rpt_family="Alu" 2176. .2372
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575. .882
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1871. .2190
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                                                                                                                                                          Submitted (08-JAN-2000) Center for Human Genome Studies, DOE Joint Genome Institute, Los Alamos National Laboratory, MS M888, Los Alamos, NM 87545, USA
                                                                                                                                                                                                                                                                                                                     Bruce, D., Mundt, M., Doggett, N., Munk, C., Saunders, E., Robinson Jones, M., Buckingham, J., Chasteen, Thompson, S., Goodwin, L., Bryant, J., Tesmer, J., Meincke, L., Longmire, J., White, S., Tatum Campbell, C., Fawcett, J., Maltbie, M., Bussod, M., Sutherland, R.,
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                           /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="16"
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/rpt_tamily="Alu" complement(1851818917) /rpt_family="Alu" complement(1875419036) /rpt_family="Alu" complement(1945619559) /note="GRAIL 2 excellent exon, frame 1" 2023920397 /rpt_family="MER20" complement(2080821104) /rpt_family="Alu"	/rpt_ramily="Alu" 1376114148 /rpt_family="Alu" 1407214371 /rpt_family="Alu" complement(1440114696) /rpt_family="Alu" 1506115366 /rpt_family="Alu" 1538315706 /rpt_family="Alu" 1538315706 /rpt_family="Alu" 1538316185) /rpt_family="Alu" complement(1619216347) /rpt_family="Alu" 1659516831 /rpt_family="Alu" 1659116831 /rpt_family="Alu" 1659116831	9965. 10332 /rpt_family="Alu" complement(10403. 10835) /rpt_family="Alu" complement(10801. 10977) /rpt_family="Alu" 11580. 11780 /rpt_family="MER42" 11803. 12101 /rpt_family="Alu" 1282. 12576 /rpt_family="Alu" 12643. 13073 /rpt_family="Alu" 12643. 13073 /rpt_family="Alu" 12643. 13073 /rpt_family="Alu" 12643. 13073 /rpt_family="Alu" 12643. 13073 /rpt_family="Alu" 12643. 13073 /rpt_family="Alu" 12643. 13073	/rpt_family="Alu" /rpt_family="Alu" /rpt_ement(68486983) /note="GRAIL 2 excellent exon, frame 1" /7473776 /rpt_family="Alu" /931. 8385 /rpt_family="Alu" 88089139 /rpt_family="Alu" 93949682 /rpt_family="Alu" 93159812 /rpt_family="Alu" 95159812 /rpt_family="Alu" /rpt_family="Alu" /rpt_family="Alu" /rpt_family="Alu" /rpt_family="Alu"	/rpt_family="Alu" 3187 . 3504 /rpt_family="Alu" complement(3571 . 3890) /rpt_family="Alu" complement(3859 . 4163) /rpt_family="Alu" 4198 . 4503 /rpt_family="Alu" 4826 . 5155 4826 . 5155 6749 6045
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ACCESSION
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Chemistry: Dye-terminator Big Dye; 94% of reads Chemistry: Dye-primer-amersham; 2% of reads Chemistry: Dye-primer Big Dye; 1% of reads Consensus quality: 136114 bases at least Q40
                                                                                   Assembly program: XGAP4; version 4.5 Sequencing vector: M13; M77815; 25% of reads Sequencing vector: plasmid; L08752; 74% of reads Chemistry: Dye-terminator ET-amersham; 0% of reads Dye-terminator ABI; 1% of reads
                                                                                                                                                                                                                                                                                                                                                                             Submitted (04-OCT-2000) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk on Aug 14, 2000 this sequence version replaced gi:9588436.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HSJ599G15 138278 bp DNA HTG 06-OCT HOMO sapiens chromosome 1 clone RP4-599G15 map p12-13.2, SEQUENCING IN PROGRESS ***, 6 unordered pieces.
                                                                                                                                                                                                                                               Contact: humquery@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                        Center project name: dJ599G15
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60.1%;
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Pred. No. 2.
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Best Local
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                        195 cccgtgcaaagagtgcggccgccgcttccggcacaaaccccaacctgctgtctcacagcaa 254
                                                                                                                                 135
                                                                                                                                                                                                                       75
                                                                                                                                                                                                                                                                                      15 cgaccgcccttccagtgtgcctgttgtggcaagcgcttccggccacaagcccaacttgat 74
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                                                                                                            ctttaccaataagccctatctgacttcgcaccggcgcatccacaccggcgagaagcccta 194
CCCGTGCCCCGAGTGCGGCGAGGCCTTCAGCCTCAGCTCGCATCTGTTGAGCCACCGGCG 94094
                                                                                                                                                                                                cyctcaccyccycytycacacygycyaycygyccccaccaytyccccyaytycygyaaycy 134
                                                                                   CTTCAGCTGGCGCGCCGACCTGCTCAAGCACCGGCGCCCTGCACACGGGCGAGAAGCCCTA 94154
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Insert size: 126614; 2.3% error; agarose-fp
Quality coverage: 6.30x in Q20 bases; sum-of-contigs Quality
coverage: 8.38x in Q20 bases; agarose-fp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NOTE: This is a 'working draft' sequence. It currently consists of 6 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   41783
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22188. .29998
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30099. .138278
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fragment_chain:1"
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fragment_chain:1"
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/clone_lib="RPCI-4"
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/db_xref="taxon:9606"
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Pred. No. 4.8e-13;
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Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,M.,

Baker,J., Baldwin,J., Barna,N., Beckerly,R., Benn,J., Brown,A.,

Castle,A., Cerny,J., Colangelo,M., Collins,S., Collymore,A.,

Cooke,P., DeArellano,K., Depayre,E., Devon,K., Dewar,K.,

Donelan,L., Doyle,M., Ferreira,P., FitzHugh,W., Forrest,C.,

Funke,R., Gage,D., Galagan,J., Gaddyna,S., Gilbert,D., Grant,G.,

Karatas,A., Lehoczky,J., Lieu,C., Locke,K., Macdonald,P.,

Marquis,N., McEwan,P., McGurk,A., McKernan,K., McLaughlin,J.,

Meldrim,J., Molla,M., Morris,W., Morrow,J., Mychaleckyj,J.,

Naylor,J., Niloff,M., O'Connor,T., O'Donnell,P., Pavlin,B.,

Naylor,J., Niloff,M., O'Connor,T., Roberts,D., Roy,A., Severy,P.,

Stange-Thomann,N., Stojanovic,N., Stone,C., Subramanian,A.,

Tesfaye,S., Torruella-Miller,I., Vassiliev,H., Vo,A., Wagner,A.,

Wheeler,J., Wu,X., Wyman,D., Ye,W.J. and Zody,M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gattcacaagcgatccgaggggtcggcccaggccgcccccggccc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (08-MAY-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Jun 24, 2000 this sequence version replaced gi:8516078. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 (bases 1 to 29802)
Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Mus musculus chromosome, clone CT7-345D4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HTG; HTGS_PHASE2
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                                                                                                                                                                                                                                                                                                                                                                               NOTE: This is a 'working draft' sequence. It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that he
                                                                                                                                                                                                                              by the finished sequence as soon as it is available and the accession number will be preserved.

1 29802: contig of 29802 bp in length.
                                                                                                                                                                                                                                                                                                                          This sequence will be replaced
                                                                                                                                                                                                                                                                                                                                                      provided by the submittor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Center project name: 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Web site:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Center code: WIBR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Center: Whitehead Institute/ MIT Center
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                           /clone_lib="CitbCJ7 Mouse BAC"
6618 c 6969 g 8161 t
                                                                                                               /organism="Mus musculus"
/db_xref="taxon:10090"
                                                                                                                                                                                                        Location/Qualifiers
                                                                                   /clone="CT7-345D4"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              http://www-seq.wi.mit.edu
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e CT7-345D4, *** SEQUENCING
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                                                                                                                                                                                                                 On May 30, 2000 this sequence version replaced gi:7249370 All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                            Peterson,K., Pollara,V., Riley,R., Roy,A., Santos,R., Severy,P., Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J., Tesfaye,S., Tirrell,A., Vassilev,H., Vo,A., Wheeler,J., Wu,X., Wyman,D., Ye,W.J., Zimmer,A. and Zody,M.
                                                                                                                                                                                                                                                                                                                       Submitted (17-NOV-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AC015887 201458 bp DNA HTG 30-MAY-2000 Mus musculus clone CT7-315E6, WORKING DRAFT SEQUENCE, 20 unordered
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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AC015887.3
                                                                                                                                                                            http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
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Contact: sequence_submissions@genome.wi.mit.edu
                                 Web site: http://www-seq.wi.mit.edu
                                                                       Center code: WIBR
                                                                                                     Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HTGS_PHASE1; HTGS_DRAFT
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Pred. No. 1.0
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Mismatches 112;
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Sequencing vector: Plasmid; n/a; %-0.f%% of reads
Sequencing vector: Plasmid; n/a; %-0.f%% of reads
Sequencing vector: Dismid; n/a; %-0.f%% of reads
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44871: contig of 13922 bp in
171: gap of 100 bp
61254: contig of 16283 bp in
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18405: contig of 3111 k
305: gap of 100 bp
20293: contig of 1788 k
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74139: contig of 12785 bp
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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                                                                                                                                                                                                                                                                                                               Sugano, Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure Analysis, Human Genome Cent Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639, Japan (E-mail:cdnal@ims.u-tokyo.ac.jp, Tel:81-3-5449-5286, Fax:81-3-5449-5416)
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sugano,S., Suzuki,Y., Ota,T., Obayashi,M., Nishi,T., Isogai,T., Shibahara,T., Tanaka,T. and Nakamura,Y.
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Sugano, S., Suzuki, Y.,
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                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (29-AUG-2000) to the DDBJ/EMBL/GenBank databases. Sumio
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/db_xref="taxon:9606"
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fis, clone COL09895, highly similar to
for AP4 zinc finger protein.
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ra,Y., Isogai,T. and Sugano,S.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Dobner,T.G.
Direct Submission
Direct Submission
Submitted (17-AUG-1999) Dobner T.G., Institut fuer Medizinische Submitted (17-AUG-1999) Dobner T.G., Institut fuer Medizinische Mikrobiologie und Hygiene, Universitaet Regensburg, GERMANY Franz-Josef-Strauss-Allee 11, 93053 Regensburg, GERMANY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dobner, T.G., Fischer, M. and Groitl, P. Cloning of a novel zinc finger protein Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HSA245553 2878
Homo sapiens mRNA
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1 (bases 1 to 2878)
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              CDRSFSQKSNLITHRKSHIRDGAFCCAICGQTFDDEERLLAHQKKHDV" 973 c 839 g 538 t
                                                    TCAECGKNFGKKTHLVAHSRVHSGERPFACEECGRRFSQGSHLAAHRRDHAPDRPFVC
PDCGKAFRHKPYLAAHRRIHTGEKPYVCPDCGKAFRQKSNLVSHRRIHTGERSYACPD
                                                                                                        /translation="MGPAQPRLLSGPSQESPQTLGKESRGLRQQGTSVAQSGAQAPGR AHRCAHCRRHFPGWVALWLHTRRCQAKLFLPCPCECGRRFRHAFTHALHRQVHAAATPD LGFACHLCGGSFRGWVALWLHTRRCQAKLFLPCPCECGRRFRHKPKQLRAHLQRCHPPA PAARPFICGNCGRSFAQWDQLVAHKKVHVABALEEAAAKVLGPRSRGRPAVTAPRPGG DAVDRPFQCACCGKRFRHKPNLIAHRRVHTGERPHQCPECGKRFTNKPYLTSHRRIHTGEKYPQCACCGKRFRHKPNLIAHRRVHTGERPHQCPECGKRFTNKPYLTSHRRIHTGEKYPQCACCGKRFRHKFNLLSHSKIHKRSEGSAQAAPGPGSPQLPAGPQESAAEPTP
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                                                                                          AVPLKPAQEPPPGAPPEHPQDP1EAPPSLYSCDDCGRSFRLERFLRAHQRQHTGERPF
                                                                                                                                                                                                                           /product="AP4 protein"
/protein_id="CAB53100.1"
/db_xref="GI:5748565"
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106. .1776
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/db_xref="taxon:9606"
/cell_line="HeLa"
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for AP4 zinc finger protein.
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             cyatccgagggtcggcccaggccgccccgggcccgggggagcccccagctgccagccggc 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (02-NOV-1999) Pathology, University of Vermont, Soule Medical Alumni Building, Burlington, VT 05405, USA Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The dhfr oribeta-binding protein RIP60 contains 15 zinc fingers: DNA binding and looping by the central three fingers and an associated proline-rich region succeed Acids Res. 28 (2), 570-581 (2000)
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1 (bases 1 to 2954)
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GPQESAAEPTPAVPLKRAQEEPPGAPEHPQOD IEAPPSLYSCDCGRSSRLERELRA
HORHDTGEREPTCAEGGKNFGKTHLVAHSPVHSGERPFACEEGGRRFSQSSHLAAHR
PDHAPDRPFVCPDCGKAFRHKPYLARHRRIHTGEKPYVCPDCGKAFSQKSNLVSHRRI
                                                                                                                                                                  {	t HTGERPYACPDCDRSFSQKSNLITHRKSHIRDGAFCCAICGQTFDDEERLLAHQKKHD}
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/db_xref="taxon:9606"
/cell_line="HeLa"
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                                                                                                                                                                                                                                                                                                                                                               /note="contains 15 C2H2-Kruppel-like zinc fingers'
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RIP60 mRNA, complete cds.
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AC005586
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99063792
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Submitted (12-JUN-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
                                                                                                                                                                                                                                                                 4 (bases 1 to 132150)
Waterston, R.H.
                                                                                                                                                                                                                                                                                                                                                                                                          2 (bases 1 to 132150)
Stoneking,T., Ozersky,P., Wohldmann,P. and Le,T.
The sequence of Homo sapiens PAC clone RP4-584D14
                                                                                                         Submitted (30-SEP-2000) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 6 On Jun 12, 2000 this sequence version replaced g1:3907529.
                                                                                                                                                                                                                                                                                                                   Direct Submission
Submitted (01-SEP-1998) Genome
University School of Medicine,
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3 (bases 1
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Sulston, J. E. and Waterston, R.
Toward a complete human genome sequence
Genome Res. 8 (11), 1097-1108 (1998)
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                                                                                                                                                            Direct Submission
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             Web site: http://genome.wustl.edu/gsc
Contact: sapiens@watson.wustl.edu
Summary Statistics
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Center project name: H_DJ0584D14
                                                              Center: Washington University Genome Sequencing Center code: WUGSC
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                                                                                                                                                                                                                                                                                                                      Louis,
                                                                                                                            USA
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NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >-This sequence was finished as follows unless otherwise noted: restriction digest.

MAPPING INFORMATION:
The sequence of this clone was established as part of convencing collaboration between the NHGRI Chromosome **7** a mapping Mapping and

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The sequence RP4-584D14 from base position 21655 to 22775 in trich. This region was sized with PCR from genomic DNA and thindili digest with band size 3643 real, and 3642 insilicosequence RP4-584D14 from base position 22628 to 22637 is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The clone sequenced to the right is RP5-820A21, 200 base pair overlap. Actual start of this clone is at base position 1 of RP4-584D14; actual end is at base position 131954 of RP4-584D14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This clone was derived from human PAC library RPCI-4, prepared by Pieter de Jong and coworkers at the Roswell Park Cancer Institute (http://bacpac.med.buffalo.edu) using the method described by Ioannou et al., Nature Genetics 6:84-9 (1994). The library is from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       one male donor.
The clone may be obtained either from Genome Systems,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mailto:egreen@nhgri.nih.gov , or see http://genome.wustl.edu/gsc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        represented by sequence derived by PCR Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (http://www.resgen.com); or from Pieter de Jong.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (http://www.genomesystems.com) or Research Genetics,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="7"
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                                                                                                 'note="match to EST
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/note="similar to Oryctolagus cuniculus EST C83534 (NID:g3062491)"
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8591. .9167
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8459. .8461
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8075. .8451
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8707. .8845
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8008. .8309
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7896. .8372
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/note="match to
7886. .8357
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/note="similar to
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ferreira, P., FitzHugh, W., Forrest, C., Funke, R., Gage, D., Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Lehoczky, J., Lieu, C., Locke, K., Macdonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K., McLaughlin, J., Meldrim, J., Morrow, J., Naylor, J., Norman, C. H., O'Connor, T., O'Donneil, P., Peterson, K., Pollara, V., Riley, R., Roy, A., Santos, R., Severy, P., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Tirrell, A., Vassillev, H., Vo, A., Wheeler, J., Wu, X., The Marchan, M., Wassillev, H., Vo, A., Wheeler, J., Wu, X., Marchan, M., Wassillev, H., Vo, A., Wheeler, J., Wu, X., Marchan, M., Wassillev, H., Vo, A., Wheeler, J., Wu, X., Marchan, M., Wassillev, H., Vo, A., Wheeler, J., Wu, X., Marchan, M., Wassillev, H., Vo, A., Wheeler, J., Wu, X., Marchan, M., Wassillev, H., Vo, A., Wheeler, J., Wu, X., Marchan, M., Wassillev, H., Vo, A., Wheeler, J., Wu, X., Marchan, M., Wassillev, H., Vo, A., Wheeler, J., Wu, X., Marchan, M., Wassillev, H., Vo, A., Wheeler, J., Wu, X., Marchan, M., Wassillev, H., Vo, A., Wheeler, J., Wu, X., Marchan, M., Wassillev, H., Vo, A., Wheeler, J., Wu, X., Marchan, M., Wassillev, H., Vo, A., Wheeler, J., Wu, X., Marchan, M., Wassillev, H., Vo, A., Wheeler, J., Wu, X., Marchan, M., Wassillev, H., Vo, A., Wheeler, J., Wu, X., Marchan, M., Wassillev, H., Vo, A., Wheeler, J., Wu, X., Marchan, M., Wassillev, H., Vo, A., Wheeler, J., Wu, X., Marchan, M., Wassillev, H., Vo, A., Wheeler, J., Wu, X., Marchan, M., Wassillev, H., Vo, A., Wheeler, J., Wu, X., Marchan, M., Wassillev, H., Vo, A., Wheeler, J., Wu, X., Marchan, M., Wassillev, H., Vo, A., Wheeler, J., Wu, X., Marchan, M., Wassillev, H., Vo, A., Wassillev, H., Wassillev, H.
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                                                                                                                                                                                                                                                                                                                                         sequencing reads that have not been assembled into contigs. Runs of N are used to separate the reads and the order in which they appear is completely arbitrary. Low-pass sequence sampling is useful for identifying clones that may be gene-rich and allows
                                                                                                                                                                                                                          will be sequenced to completion.
                                                                                                                                                                                                                                                                        overlap relationships among clones to be deduced. However, it should not be assumed that this clone
                                                                                                                                                                                                            the record
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: sequence_submissions@genome.wi.mit.edu
------ Project Information
Center project name: L3769
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Eutheria;
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944: gap of 100 bp
1799: contig of 855 bp in length
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contig of 855 bp in length of 100 bp
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3871: gap
       36578: contig of 875
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17269: con
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12520: gap of 100 bp
13422: contig of 902 bp in
13522: gap of 100 bp
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20160: contig of 868 bp
0)260: gap of 860 bp
21120: contig of 860 bp
1220: gap of 100 bp
22076: contig of 856 bp
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29827: cont
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19192: ~
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34638: contig of 876
38: gap of 100 b
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28859: contig of 868 bp
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27891: contig of 875
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14382: contig of 860 bp in
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8596:
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7617:
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30828: contig
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51027: contig of 852 bp
51127: gap of 100 bp
                                                                                                                           63425: gap of 100 bp
64283: contig of 858 bp in
64383: gap of 100 bp
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57786: contig of 893 bp
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58511: contig of 625 bp
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61400: contig of 861
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54858: contig of 851 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                      49112: contig of 864 bp 112: gap of 100 bp 50075: contig of 863 bp 75.
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                                                                                               66214: contig of 854 bp in
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43246: contig of
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44206: contig of 860
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 (bases 1 to 244410)
1 (bases 2 to 244410)

* NOTE: Estimated insert size may differ from sequence length 
* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (22-MAY-2000) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Jul 25, 2000 this sequence version replaced gi:8468712.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          244410 bp DNA HTG 25-JUL-20. Homo sapiens chromosome 12 clone RP11-665J20, WORKING DRAFT SEQUENCE, 28 unordered pieces.
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Direct Submission
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                                                                                                                                                                                       Center project name: HAVI
Center clone name: RP11-665J20
Center clone name: RP11-665J20
Center clone name: Phrap; version 0.990329
Assembly program: Phrap; version 0.990329
Consensus quality: 208190 bases at least Q40
Consensus quality: 224572 bases at least Q20
Consensus quality: 231987 bases at least Q20
Estimated insert size: 219523; sum-of-contigs estimation Quality coverage: 0x in Q20 bases; agarose-fp estimation Quality coverage: 5.8x in Q20 bases; sum-of-contigs estimation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Web site: http://www.hgsc.bcm.tmc.edu/
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BASE COUNT
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                          /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="12"
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Query Match

29

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Score 52.4;

DВ

58;

Length 244410;

\* sequencing reads that have not been assembled into \* contigs. Runs of N are used to separate the reads \* and the order in which they appear is completely

NOTE: This record contains 72 individual

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REFERENCE
AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Grand-Pierre, N., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J.C., Illev, I., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., LaRocque, K., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPheeters, R., McCarthy, M., McEwan, P., McGurk, A., McKernan, K., Menpey, V., Morrow, J., Murphy, T., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Olivar, T.M., Oliver, J., Peterson, K., Pierre, N., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Tirrell, A., Travers, M., Trigilio, J., Vassillev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J., Zimmer, A. and Zody, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cagagcacccgcaggacccgatcgaagcccccccctcc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N., Anderson,S., Baldwin,J., Barna,N., Bastien,V., Beda,F., Boguslavkly,L., Boukhgalter,B., Brown,A., Burkett,G., Campopiano,A., Castle,A., Choepel,Y., Colangelo,M., Collins,S., Colongelo,M., Colongelo,M.,
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                                                                                                                                                                                                                                                                                                                                                                                                   All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (07-APR-2000) Whitehead Institute/MIT Center Research, 320 Charles Street, Cambridge, MA 02141, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Dodge, S., Domino, M., Doyle, M., Ferreira, P., FitzHugh, W., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished
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Birren,B., Linton,L.,
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Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AC036107
                                                                                                                                                                                                                                                                                                                                                  http://ftp.genome.washington.edu/RM/RepeatMasker.html
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Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L2373
Center clone name: 311_K_17
                                                                                                                                                                               Web site: http://www-seq.wi.mit.edu
                                                                                                                                                                                                                        Center: Whitehead
Center code: WIBR
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                                                                                                                                                                                                                                                                     Institute/ MIT Center for Genome
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0; Mismatches
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                                                                                                                                                                                                                                                                     Research
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arbitrary. Low-pass sequence sampling is useful for identifying clones that may be gene-rich and allows overlap relationships among clones to be deduced. However, it should not be assumed that this clone will be sequenced to completion. In the event that the record is updated, the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              preserved.
                       J 26549: gap or 0 27407: contig c
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13 1782: gap of
3 2579: contin 7
20281: contig (
2 28381: gap of
2 29164: contin
                                                                                                         23021;
2 23121; gap
                                                                                                                                                                                               7 16876: gap of 10
7 17672: contig of 7
3 17772: gap of 10
18553: contig of 7
                                                                                                                                                                                                                             1407i: contig c
2 14171: gap of
2 14981: contig c
2 15081: gap of
2 15094: contig c
5 16004: gap of
5 16776: contig
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3 12284: contig of
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Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Roy,A., Santos,R., Schauer,S., Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J. Tesfaye,S., Theodore,J., Tirrell,A., Travers,M., Trigilio,J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barna, N., Bastien, V., Beda, F., Boguslavkiy, L., Boukhgalter, B., Brown, A., Burkett, G., Campopiano, A., Castle, A., Choepel, Y., Colangelo, M., Collins, S.,
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HOMO sapiens clone RP11-24J1, LOW-PASS SEQUENCE SAMPLING.
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NOTE: This record contains 158 individual sequencing reads that have not been assem contigs. Runs of N are used to separate t
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                                                                                                                                                                              Center project name:
                                                                                                                                                                                                                                            Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                              Web site: http://www-seq.wi.mit.edu
                                                                                                                                                                                                                                                                                                                       Center: Whitehead Institute/ MIT Center code: WIBR
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                                                                                                                                                                                                                   Project Information
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and the order in which they appear is completely arbitrary. Low-pass sequence sampling is useful for identifying clones that may be gene-rich and allows
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             will be sequenced to completion. In the event that
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30 24829: gap of 100 bp
25580: contig of 751 bp i
1 25680: gap of 100 kp
1 26431
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94 10150: contig of 757 bp in le
95 10250: gap of 100 bp
51 11029: contig of 779 bp in le
30 11129: gap of 100 bp
30 11189: contig of 760 bp in le
90 11989: contig of 770 bp in le
90 11759: contig of 770 bp in le
90 12759: contig of 770 bp in le
10 12859: gap of 100 bp
13613: contig of 754 bp in le
14 12779: contig of 754 bp in le
100 b<sub>k</sub>
2/290: contig of 759 b
11 27390: gap of 100 hr
1 28142: conti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           59 15319: contig of 761 bp 1
20 15419: gap of 100 bp
20 16181: contig of 762 bp 1
22 16281: gap of 100 bp
32 1738: contig of 757 bp 1
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6744: /
                                                                            25680: gap of 100 bp
26431: contig of 751 bp
26531: gap of 100 bp
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1/890: contig of 752 bp ii
7990: gap of 100 km
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56304: contig of 757 bp
5404: gap of 100 bp
57169: contig of 765 bp
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5044: gap of 100 bp
35820: contig of 776 bp i
5920: gap of 100 bp
36680: contig of 760 bp i
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2497: contig of 739 bp 1
2497: gap of 100 bp
33255: contig of 758 bp 1
33255: gap of 100 bp
34094: contig of 739 bp 1
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54597: contig of 741 bp
197: gap of 100 bp
55447: contig of 750 bp
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132: gap of 100 bp
30688: contig of 756 bp
788: gap of 100 bp
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                            arbitrary. Low-pass sequence sampling is useful for identifying clones that may be gene-rich and allows overlap relationships among clones to be deduced. However, it should not be assumed that this clone
                                                                                                                                                           NOTE: This record contains 81 individual sequencing reads that have not been assembled into contigs. Runs of N are used to separate the reads and the order in which they appear is completely
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                                                                                                                                                                                                                                                                                                                                     Center project name: L3938
Center clone name: 20_M_3
                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Center code: WIBR
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Colney, Norwich, No
Notes:
Streptomyces coelic
                                                                                                                       are also included but some of these may be fortuitous. The length in codons is given for each CDS.

The length in codons is given for each CDS.

Usually the highest scoring match found by fasta -o is given for CDS which show significant similarity to other CDS in the database. The position of possible ribosome binding site sequences are given where these have been used to deduce the initiation codon.

Gene prediction is based on positional base preference in codons using a specially developed Hidden Markov Model (Krogh et al., Nucleic Acids Research, 22(22):4768-4778(1994)) and the FramePlot program of Bibb et al., Gene 30:157-66(1984) as implemented at http://www.nth.com/
http://www.nih.go.jp/
http://www.nih.go.jp/
jun/cgi-bin/frameplot.pl. CAUTION: We may not have predicted the
correct initiation codon. Where possible we choose an initiation
codon (atg, gtg, ttg or (att)) which is preceded by an upstream
ribosome binding site sequence (optimally 5-13bp before the
                                                                                                                                                                                                                                                                                                                                                                                             available on the World Wide Web. (URL; http://www.sanger.ac.uk/Projects/S_coelicolor/) CDS are numbered using the following system eg SC7B7.01c. coelicolor), 7B7 (cosmid name), .01 (first CDS), c (complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (04-FEB-2000) Streptomyces coelicolor sequencing project, Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA E-mail: barrellesanger.ac.uk Cosmids supplied by Prof. David A. Hopwood, [3] John Innes Centre, Norwich Research Park,
                                                                                                                                                                                                                                                                                                                                    The more significant matches with motifs in the PROSITE database are also included but some of these may be fortuitous.
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Streptomyces coelicolor A3(2)
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A set of ordered cosmids and a detailed genetic and physical map
for the 8 mb Streptomyces coelicolor A3(2) chromosome
Mol. Microbiol. 21 (1), 77-96 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 (bases 1 to 8058)
Redenbach, M., Kieser, H.M.,
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                'product="hypothetical protein SCE56.03c"
                                                              /codon_start=1
                                                                                  /note="SCE56.03c,
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len:

260

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upstream initiation codon.

IMPORTANT: This sequence MAY NOT be the entire insert sequenced clone. It may be shorter because we only sequenced clone. It may be shorter because we arrange the sequenced clone.
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Cosmid E56 Overlaps cosmid E59 on the AseI-E ge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         initiation codon).
                                                                                                                                                                                                                                                 /translation="MRYIRLGTTGLEVSAIALGCMGFGEPDRGGEPWSLGADPSRDII
RQALEGGVNFLDTANGYSAGNSEIVGADAVKOPARREEVVLSTKVWMRNRPGPNGAGL
SRKAIFAELDASLKRLGTDYIDLYGLIRWDVDTPIEFETLEALHDVVKSGKVRVLGASS
MYAWQFAKALYLADLNGWTRFVSMQDHYNLIHREAEREMLPLCADQGIGVIFWSPLAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      coelicolor putative aldo/keto reductase (fragment) SCF81.28c, 307 aa; fasta scores: opt: 1370 z-score: 1572.6 E(): 0; 65.2% identity in 305 aa opt: 10 sw:NORA_ASPFL (EMBL:132377) Aspergillus flavus norsolorinic acid reductase (EC 1.1.1.-) NorA, 388 aa; fasta scores: opt: 572 z-score: 659.1 E(): 2.7e-29; 32.8%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note-"SCE56.02, possible oxidoreductase, len: 336 similar to TR:CAB61562 (EMBL:ALI33171) Streptomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="SCE56.02"
904. .1914
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="SCE56.01c"
899. .902
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                                                           complement(1881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /translation="MTVPEPRDTDVAAPVEPALAPAAPAETVLSRAYRALSIGIVSVI
VLIAFEATAVGTAMPVAARELDGVSLYAFAFSGYFTTSLFGMVLSGQWSDRRGPLAPL
TTGIATFAAGLVLSGTAGAMMLFILGRAVQGFGGGLVIVALYVVVGRAYPERLRPAIM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contains possible hydrophobic membrane spanning regions" /codon_start=1
/gene="SCE56.03c"
/note="scre
                                                                                                                                                                                         VVTSPIVGVTKPAQLADAIAAVDVGLDEDEAAYLEEPYQPHEAAYLEESFYKARPAAA
                                                                                                                                                                                                                          GRLTRARDTATARAGTDEGGRILYRDEDQAVAERVREIAGRRGLSPAQVALAWVMRNP
                                                                                                                                                                                                                                                                                                                                                                               /product="putative oxidoreductase"
/protein_id="CAB72221.1"
/db_xref="GI:6912006"
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/protein_id="CAB72220.1"
/db_xref="GI:6912005"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /transl_table=11
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identity in 329 aa overlap"
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/db_xref="taxon:100226"
/clone="cosmid E56"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="SCE56.02"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="SCE56.01c, possible transport protein (partial),
len: >170 aa; similar to TR:AAF11647 (EMBL:AE002045)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="SCE56.01c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /partia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              organism="Streptomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      If this cannot be identified we choose the most
                                                                            5.03c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 coelicolor A3(2)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ŝ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         coelicolor cosmid SCE19A"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            genomic restriction
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gene CDS

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/note="Pfam match to entry PF01315 Ald_Xan_dh_C, Aldehyde oxidase and xanthine dehydrogenase, C terminus, score 279.60, E-value 3.9e-80" complement(5075. .7396) gene="SCE56.05c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note-"SCE56.04c, possible oxidoreductase, len: 773 aa; similar to TR:Q92BN7 (EMBL:AL034492) Streptomyces coelicolor putative oxidoreductase SC65.08, 828 aa; fast scores: opt: 1088 z-score: 1144.8 E(): 0; 42.2% identity 1782 aa overlap and to SW:XDH_DROPS (EMBL:M33977)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="SCE56.04c"
/note="SCE56.04c, possib
similar to mn ^^
                                                                 STASGPGEGHGPGPAASVHGHDPAVSPDGPRPADGSYAHAPGVDTQSAAGAAGAGAGPGV
RAPDGAPEGSGTATDGPRGAEEDAEGFRKSAGGPEBAARGSFREAEGFVTDRAPTA
GRERRAPEPAGEHGQAPEGEPRESPAAPGGVPADASDRADSDDPADPADPTDPTDPTDPT
RGTDAADAGSGADGPEAVTDGVPDAAQEPSAPAGPQDEHPLASYVLRVNGADRPVTDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="SCE56.05c, unknown, len: 773 aa. High content in proline, glycine and alanine. Contains Pfam matches to entries PF00111 fer2, 2Fe-2S iron-sulfur cluster binding domains and PF01799 fer2.2, [2Fe-2S] binding domain and match to Prosite entry PS00197 2Fe-2S ferredoxins, lines.sulfur binding region signature"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement(2943. .4955)
/gene="SCE56.04c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LARQIVQDTLGVDEVQVAPVDTDQPPAGPGCRGRHTWYSGGAVERAAKMYRTQLLQPL
AHQFGMSTELLQIADGKITSYDGVLSTTVTEALDGKELWATAQCRPHPTEPLDEAGQG
DAFVGMAFCAIRAVVDVDIEIGSVRVVELAVAQDVGRVLNPAQLTARIEAGVTQGVGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGQADRPVFASEAVRHHGEPLAAVAADHPDTARMAAAAVIVEYELLDPVTDPEQAFEA
EPLHPDGNLIRHIPLRHGDPDAAGEIVVEGLYRIGRQDPAPIGAEAGLAVPRPDGGVE
LYLASTDPHGDRDIAAACYGLSPEQVKIVVTGVPGATADREDQGFQLPLGLLALKTGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HPLYSDYSALALTLWALRRAGRLETSAGGGPDYREAAAGRAL"
complement(2757. .5078)
gene="SCE56.04c"
                                                                                                                                                                                             GTGAPATLPGGAPAPWATQPAGQPWGEDAPRPGPAGPADEERPAASGHAYGATATGHG
EGHGADAGHRADADLSGYGPGHDSGADAGHGPDAAVGPHGPGPSAPGAGPVPHAHGPG
                                                                                                                                                                                                                                                                                     /translation="MTDDQHGDPHGDQHGQGTPPGGSRWDPLPQGDYDDGATAFYKLP
EGGVDALLASSDSPLAAPGHGYVPPQITVAPATTAGTDPAATGSWAAPSAPSAPVDGT
QWQVPDAGQDPAAHQGYGGYPAQQDPYGGAAPYDVHAGQGAPGHDDRFAYQPGPTGQW
                                                                                                                                                                                                                                                                                                                                                                             /product="hypothetical protein SCE56.05c"
/protein_id="CAB72224.1"
/db_xref="GI:6912009"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="SCE56.05c"
/note="scrs(")
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ASPAAVASAVRAATGRPVNRLPIRPQAAVATGH"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PVKLTATREESFLGHTHRHPTLLRYRHHADABGRIVKVEAQILLDAGAYADTSSDALA
AAVAFACEPYVVPNAFIEGWAVRTNNPPSGHVRGEAMQVCAAXEAQMOKVAKKLGLD
PABVRLRNVLATGDVLPTGOTVTCBARVAELLAVRDEPLPALPKDPPEBEWLLFGED
EGAGEPGAVRRGVGYGIGMVHMLGAEGADEVSTATVKVQGGVATVLCAAVETGQGFTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="putative oxidoreductase"
/protein_id="CAB72223.1"
/db_xref="gI:6912008"
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Rtavpslvtryrlatyvedpartrdaarrpgasgersbuwitstlmsgllllayshrae
Pgtsrdlpprfldrefgrtwtrfedidfprthefgreflætglebarpfrlb
DDLPLPTLAEYGEEHPDQPVPPGADHLVRLGRLADGAHVAVDGTTGAVLTwrtpdgtl
                                                                                                                                                                                                                                                       dfsqaaqaaqasraeadaaaarqasgqdvtgqwsipvadgdlpdesgefttsslaeqw
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation="mSNDAATAEAEGTAEAATPVPDP1PHGLGASLPPADARAKTEGT
FPYAADLMAEGLLMAAVLRSPHPRARIVSIDTTHAREMPGVRAVVTHEDVPGSPLHGR
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/db_xref="GI:6912007"
                                       WIGESLLYVLRERLGLAGAKDGCSQGECGACNVQVDGRLVASCLVPSVTAAGSEVRTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /transl_table=11
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/transl_table=11
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RESULT 11
AP001052/c
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ORIGIN
                                                          Db 113151 CCCCGCGAGCCCCCCGCGAGCCCCCGCGAGCCCCCGCGAGCCCCCGCGAGCCCCC
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Best Local S
Matches 87
                                                                                                                                                                                                                      Query Match
Best Local
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caggggccccgccagagcacccgcaggacccgatcgaagccccccc 170
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               agcccacccggcggtacctctgaaaccggcccaggagccgccgccagggggccccgccag 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             aggccgccccgggcgggagcccccagctgccagccggccccccaggagtccgcggccg
                                                                                         aggagtccgcggccgagcccaccccggcggtacctctgaaaccggcccaggagccgccgc 124
                                                                                                                                                                ccgagggtcggccaggccgcccggcccggggagccccagctgccagccggcccc
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87; Conserv
                                                                                                                                                                                                         l Similarity
93; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 (bases 1 to 145540)
Shimizu, N., Kudoh, J. and Shibuya, K.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (12-JAN-2000) to the DDBJ/EMBL/GenBank databases. Nobuyoshi Shimizu, Keio University, School of Medicine, Molecular Biology; 35 Shinanomachi, Shinjuku-ku, Tokyo 160-8582, Japan (E-mail:nshimizu@dmb.med.keio.ac.jp, Tel:81-3-3351-2370,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fax:81-3-3351-2370)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens genomic DNA, chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 145540)
Shimizu, N., Kudoh, J. and Shibuya, K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens pre-pro-B cell cell_line:FLEB14-14 DNA, clone_lib:Keio
BAC library clone:KB22A5.
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Homo sapiens genomic DNA,
region, complete sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Published Only in DataBase (2000) In
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
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                                                                                                                                                                                                                                                                                                             /clone="KB22A5"
/clone_lib="Keio BAC library"
/36783 c 36979 g 35786 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
1. .145540
                                                                                                                                                                                                                                                                                                                                                                         /cell_type="pre-pro-B cell"
/chromosome="21"
                                                                                                                                                                                                                                                                                                                                                                                                            /cell_line="FLEB14-14"
                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
                                                                                                                                                                                                                        27.8%;
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                                                                                                                                                                                                         0;
                                                                                                                                                                                                     Score 49.2; DB 48;
Pred. No. 3.5;
0; Mismatches 73;
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Pred. No. 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hattori, M., Fujiyama, A., Taylor, T.D., Watanabe, H., Yada, T., Park, H.S., Toyoda, A., Ishii, K., Totoki, Y., Choi, D.K., Soeda, E., Ohki, M., Takagi, T., Sakaki, Y., Taudien, S., Blechschmidt, K., Polley, A., Menzel, U., Delabar, J., Kumpf, K., Lehmann, R., Patterson, D., Reichwald, K., Rump, A., Schillhabel, M., Schudy, A., Zimmermann, W., Rosenthal, A., Kudoh, J., Shihuya, K., Kawasaki, K., Asakawa, S., Shintani, A., Sasaki, T., Nagamine, K., Mitsuyama, S., Antonarakis, S.E., Minoshima, S., Shimizu, N., Nordsiek, G., Hornischer, K., Barandt, P., Scharfe, M., Schoen, O., Desario, A., Reichelt, J., Kauer, G., Bloccker, H., Ramser, J., Beck, A., Klages, S., Hennig, S., Riesselmann, L., Dagand, E., Wehrmaeyer, S., Borzym, K., Gardiner, K., Nizetic, D., Francis, F., Lehrach, H., Reinhardt, R. and
* Innestrasse 73, D-14195 Berlin, (
* e.mail: info-chr21@molgen.mpg.de
* URL: http://chr21.rz-berlin.mpg.d
AL163297: Submitted (10-Apr-2000)
                                                                                                                                                                                                                                                                         160-8582, Japan,
* e.mail: nshimi
* URL: http://ww
                                                                                                                                                                                                                                                                                                                                                                                                                  * Institute of Molecular Biotechnology, Genome Analysis, Beutenbergstrasse 11, D-07745 Jena, Germany, * e.mail: gscj-submit@genome.imb-jena.de
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              On May 30, 2000 this sequence version replaced gi:7717416. The chromosome 21 mapping and sequencing consortium consisting *RIKEN Genomic Sciences Center, Human Genome Research Group, *Sagamihara 228-8555, Japan,
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                                                                                                                                                                     * GBF, Dept. of Gen
* Mascheroder Weg
info.genome@gbf.de
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AP001752 AL163297 BA000005
AP001752.1 GI:7768757
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The DNA sequence of human chromosome 21.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      e.mail: hattori@gsc.riken.go.jp
URL: http://hgp.gsc.riken.go.jp/
                                                                                                                                                                                                                                                                                                                                             Keio University School of Medicine, Molecular Biology,
                                                                                                                                                                                                                                                                                                                                                                                           URL: http://genome.imb-jena.de/
                                                                                              Max-Planck Institute for Molecular Genetics,
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  http://chr21.rz-berlin.mpg.de/
97: Submitted (10-Apr-2000).
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                                                                                                                                                                                                                                                                   il: nshimizu@dmb-med.keio.ac.jp
http://www.dmb.med.keio.ac.jp/
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    D-38124 Braunschweig, Germany,

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K., Soeda,E.,
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/rpt_type=DISPERSED
6530...7150
                                           /product="heat shock transcription factor 2 binding
protein"
                                                                                                                                       complement(join(<7441. .7566,23941. 37908. .38011,50206. .50356,51680.
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/organism="Homo sapiens"
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ILNGEVLESFQKLKIVEKNLERKEQELEQLKMDCEHFKARLETVQADNIREKKEKLAL
RQQLNEAKQQLLQQAEYCTEMGAAACTLLWGVSSSEEVVKAILGGDKALKFFSITGQT
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37908. .38011,50206. .50356,51680. .51715))
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /protein_id="BAA95539.1"
/db_xref="GI:7768758"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="HSF2BP"
                                                                                                                                                                                                                                                                                                        rpt_family-"LINE/L1"
                                                                                                                                                                                                                                                                                                                                                                                   rpt_family="SINE/Alu"
                                                                                                                                                                                                                                                                                                                                                                                                                                                            rpt_family="SINE/Alu"/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     rpt_family="LTR/MaLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /rpt_family="DNA/MER2_type"
/rpt_type=DISPERSED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 rpt_family-"SINE/Alu"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="HSF2BP"
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                                                                                                                                                                                          Score 49.2; DB Pred. No. 2.3; 0; Mismatches
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                                                                                                                                                                                                                                DB 48;
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                                                                                                                                                                                                                              Length 340000;
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                                                                                                                                                                                          0;
                                                                                                                                                                                            0,
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                               sequencing reads that have not been assembled into contigs. Runs of N are used to separate the reads and the order in which they appear is completely arbitrary. Low-pass sequence sampling is useful for identifying clones that may be gene-rich and allows overlap relationships among clones to be deduced. However, it should not be assumed that this clone will be sequenced to completion. In the event that
                                                                                                                                                                                                                                                                                                       NOTE: This record contains 74 individual
                                                                                                                                                                                                                                                                                                                                          Center: Whitehead Institute/ MIT Center code: WIBR
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Web site: http://www-seq.wi.mit.edu

Center for Genome

preserved.

is updated, the accession number will

1 793: contig of 793 bp in length
794 893: gap of 100 bp
1788 2572: contig of 785 bp in length

2572: contig of 2672: gap of 1

100 bp of 785 bp in length

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Anderson, S., Baldwin, J., Barma, N., Beda, F., Boguslavkly, L.,
Boukhgalter, B., Brown, A., Burkett, G., Campopiano, A., Castle, A.,
Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P.,
DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Domino, M., Doyle, M.,
Fenestor, J., Ferreira, P., FitzHugh, W., Forrest, C., Gage, D.,
Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L.,
Grand-Pierre, N., Grantt, G., Hagos, B., Heaford, A., Hotton, L.,
Grand-Pierre, N., Grantt, G., Hagos, B., Heaford, A., Hotton, L.,
Kiein, J., Landers, T., Largocque, K., Lehoczky, J., Levine, R.,
Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., McCarthy, M.,
McEwan, P., McGurk, A., McKernan, K., McPheeters, R., Meddrim, J.,
McEwan, P., McGurk, A., McKernan, K., McPheeters, R., Meddrim, J.,
Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Olivar, T.M.,
Peterson, K., Pierre, N., Pisani, C., Pollara, V., Raymond, C.,
Riley, R., Rogov, P., Rothman, D., Roy, A., Santos, R., Schauer, S.,
Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N.,
Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Tirrell, A.,
Travers, M., Trigilio, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B.,
Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J., Zimmer, A. and
Submitted (28-FEB-2000) Whitehead Institute/MIT Center Research, 320 Charles Street, Cambridge, MA 02141, USA All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N., Anderson,S., Baldwin,J., Barna,N., Beda,F., Boguslavkiy,L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 (bases 1 to 65523)
Birren,B., Linton,L., Nusbaum,C. and Lander,E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AC024266.1 GI:7107792
HTG; HTGS_PHASE0.
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                                                                                                                                                                                          Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens, clone RP11-115F10
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27.9836: gap c

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length

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length

1 7133: gap 4 4 7941:

8041:

contig contig

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1: gap \_8832:

6242: gap 7033:

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contig contig contig of contig of

00 bp 744 bp in

length length

5398: gap 6142:

7 3586: gap 1 7 4391: gap 1 2 4491: gap 5298:

c 807

bp in

3486: 3586: gap

7.9836: gap of 100
7.10619: contig of 7
1010719: gap of 10
1010719: gap of 10
11503: contig of 7
44 11603: gap of 10
44 11603: gap of 17
71426: gap of 17
71426: gap of 17
713201: contig of 7
13201: contig of 7
13201: gap of 10

100 bp of 784 bp in

length

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13201: contig of 775 bp in length
13202 13301: gap of 100 bp
302 14085: contig of 784 bp in length
306 14185: gap of 100 bp
86 14981: contig of 796 bp in length
82 15081: gap of 100 bp
12 15879: contig of 796 bp in length
10 15879: contig of 796 bp
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Best Local S
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 21103
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caccccggcggtacctctgaaaccggcccaggagccgccgccaggggccccgccagagca 143
                                       cgcccccggcccggggagcccccagctgccagccggcccccaggagtccgcgggccgagcc 83
                                                                                 88; Conservative
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21 53220: gap of 10
31 53973: contig of 75
4 54073: gap of 100
4 54862: contia of 70
1 54060:
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2 58451: cont
2 58551: gap of
2 59333: cont
                                                                                                                                                                                                                                   3 54962: gap of 10

3 55747: contig of 7

3 55847: gap of 10

8 56660: contig of 8

1 56760: gap of 10

2 57571: contig of 8
                                                                                                                                                                                                                                                                                                                                                                                    0 48769: gap of 10
0 49560: contig of 7
1 49660: gap of 10
1 50399: contig of 7
0 50499: gap of 10
0 51301: contig of 8
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40734: contin ~ 4082'
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45162: contig of 743
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44319: contig
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38157: con
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57.1%;
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46913: cont
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334: gap of 1
41594: contig of
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43390: contig of 793
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42497: contig of 803
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contig of 826 bp
                                                                                 Score 49; DB 5
Pred. No. 5.5;
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f_811 bp in
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f 793 br
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f 802 bp in length
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f 777 bp in
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17645: contig of 8 16 17745: gap of 10 18541: contig of 7 12 18641: gap of 10 19447: contig of 8 19547: gap of 10 18 19547: gap of 10 18 20376: contig of 8 20376: contig of 8 20376: gap of 10 21179: gap of 10 21279: gap of 10 22064: contig of 7

0 15979: gap of 10 16745: contig of 16845: gap of 116845: contig of 17645: contig of 17645:

100 bp 796 bp in 100 bp

length

800

bp in length

65 22164: gap of 100 bp
65 22935: contig of 771 bp in le
65 22935: contig of 771 bp in le
65 23935: gap of 100 bp
36 23851: gap of 100 bp
36 23851: gap of 100 bp
52 23951: gap of 100 bp
52 24827: contig of 876 bp in le
52 24927: gap of 100 bp
62 25988: contig of 771 bp in le
63 25988: contig of 788 bp in le
64 2686: gap of 100 bp
67 27505: contig of 819 bp in le
68 26686: gap of 100 bp
68 27605: gap of 100 bp
68 27605: gap of 100 bp
69 25686: contig of 819 bp in le
60 27605: gap of 100 bp
60 27606: gap of 100 bp
61 27605: gap of 100 bp
62 27606: gap of 100 bp
63 27606: gap of 100 bp
64 27606: gap of 100 bp
65 27606: gap of 100 bp
66 27605: gap of 100 bp
67 27606: gap of 100 bp
68 27606: gap of 100 bp

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length length

87 26686; gap of 100 bp 177505; contig of 819 bp 17 27505; contig of 819 bp 17 27505; contig of 819 bp 17 27505; contig of 803 bp 17 27506; contig of 786 bp 17 27509; contig of 786 bp 17 27509; contig of 787 bp

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34685: gap of 35469: con

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Direct Submission
Submitted (07-FEB-2000) Whitehead Institute/MIT Center for Genome Submitted (07-FEB-2000) Whitehead Institute/MIT Center for Genome Submitted (07-FEB-2000) Whitehead Institute/MIT Center for Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DeArellano, K., Dewar, K., Domino, M., Doyle, M., Fenestor, J., Ferreira, P., Fitzhugh, W., Forrest, C., Gage, D., Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L., Gardyna, S., Grant, G., Hoylos, B., Heaford, A., Horton, L., Karatas, A., Klein, J., Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Landers, T., Lehoczky, J., Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K., McDwan, P., McGurk, A., McKernan, J., McDwan, D., McDwan, C.H., O'Connor, T., O'Donnell, P., Olivar, T.M., Peterson, K., Pierre, N., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rothman, D., Pierre, N., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rothman, D.,
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Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequencing reads that have not been assembled into contigs. Runs of N are used to separate the reads and the order in which they appear is completely arbitrary. Low-pass sequence sampling is useful for identifying clones that may be gene-rich and allows overlap relationships among clones to be deduced.
                                                                                                                                                                                                                                                                                                                                                                                         However, it should not be assumed that this clone will be sequenced to completion. In the event that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NOTE: This record contains 83 individual
                                                                                                                                                                                                                                                                                                                                                             the record
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Center clone name: 565_K_18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Web site: http:/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Center code: WIBR
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of 767 bp in
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7803:
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4300:
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25: gap of 100 k
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67: gap of 100 bp
13940: contig of 773 bp in
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22629: contig of 749 bp
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19996: contig of 787 bp
96: gap of 100 bp
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18243: contig of 773 bp in
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17370: contig of 754 bp in
6: gap of
14837: contig
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966: contig of 775 b
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15181 45280: gap of 100 bp
15281 46049: contig of 769 bp in length
1505 46149: gap of 100 bp
150 46911: contig of 769 bp in length
151 47011: gap of 100 bp
152 47011: gap of 100 bp
164 47839: contig of 828 bp in length
165 48720: contig of 77°
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24 51423; gap of 100 bp
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26 52307; gap of 100 bp
8 53069; contig of 762 bp in length
70 53169; gap of 100 bp
70 53935; contig of 766 bp in length
8 54035; gap of 100 bp
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136 54797; contig of 762 bp in length
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36674: gap of 100 hp
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49670: gap of 100 bp
50454: contig of 784 bp in length
50561: gap of 100 bp
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58389: contig of 776 bp in
58489: gap of 100 bp
59250: contig of 761 bp in
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44316: contig of 658 bp
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45180: contig of 764 bp
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35807: gap of
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56668: contig of 755 b

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57513: contig of 745 bj

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AC027375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Tirrell, A., Travers, M., Trigilio, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J., Zimmer, A. and Zody, M.
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Grand-Pierre, N., Grant, G., Hagos, B., Heatord, A., Horton, L.,
Howland, J.C., Iliev, I., Johnson, R., Jones, C., Kann, L., Karatas, A.,
Klein, J., LaRocque, K., Lamazares, R., Landers, T., Lehoczky, J.,
Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N.,
McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPheeters, R.,
McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPheeters, R.,
McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPheeters, R.,
McCarthy, Meneus, L., Mihova, T., Miranda, C., Mlenga, V., Morrow, J.,
Murphy, T., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P.,
O'Neil, D., Olivar, T.M., Oliver, J., Peterson, K., Pierre, N.,
Divar, J., Raymond, C., Riley, R., Rogov, P., Rothman, D.,
Pisani, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (30-MAR-2000) Whitehead Institute/MIT Center Research, 320 Charles Street, Cambridge, MA 02141, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Campopiano, A., Castle, A., Choepei, Y., Colangelo, M., Collir Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S.
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Boguslavkiy,L., Bounney

Boguslavkiy,L., Castle,A.,

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Birren, B., Linton, L.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                sequencing reads that have not been assembled into configs. Runs of N are used to separate the reads and the order in which they appear is completely arbitrary. Low-pass sequence sampling is useful for identifying clones that may be gene-rich and allows overlap relationships among clones to be deduced. However, it should not be assumed that this clone will be sequenced to completion. In the event that
                                                                                 be preserved.
                                                                                                                                                                                                                                                                                                                                                                   NOTE: This record contains 80 individual
                                                                                                           the record is updated, the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (bases 1 to 68581)
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                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: sequence_submissions@genome.wi.mit.edu
------ project Information
Center project name: L5319
Center clone name: 7_E_17
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t, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Web site: http://www-seq.wi.mit.edu
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Eutheria; Primates;
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                                                          720:
                                              contig of 720 bp in length
of 100 bp
contig of 773 bp in length
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6916:

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119 48218: gap of 100 bp
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119 4894: contig of 758 b
119 48934: contig of 758 b
120 49834: contig of 758 b
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52451: gap of 100 k
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9690 19789:

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100 bp f 779 bp

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18926: 18054: 17195: 16376: 15522: 14668: 13794:

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5376: gap of 1 17095: contig of 7195: gap of 1 17954: contig of

719

bp in length

gap of 76: contig of

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2405; gap of 100 bp 23162; contig of 757 b) 3262; gap of 100 bp 240400; contig of 778 b) 414040; contig of 778 b) 424040; contig of 774 b) 4989; gap of 100 bp 25763; contig of 774 b) 5863; gap of 100 bp 26646; contig of 783 b 6746; gap of 100 bp 27508; contig of 762 b 7608; gap of 100 bp 28367; contig of 759 b 8467; gap of 100 bp 29245; contig of 778 b 9345; gap of 100 bp 10014; gap of 10015; gap of 10015

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100 bp f 757 bf

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2306 22405:

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bp in

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Search completed: February 22, 2001, 03:12:23 Job time: 14801 sec

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1: gb_ba1:
2: gb_ba2:
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4: gb_ov:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIE

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NEDO human cDNA sequencing project inpublished (2000)
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Sugano,S., Suzuki,Y., Ota,T., Obayashi,M., Nishi,T., Shibahara,T., Tanaka,T. and Nakamura,Y.
                                                                                                                                                                                                             NEDO human cDNA sequencing project supported by Ministry of International Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology; cDNA library construction, 5'- & 3'-end one pass sequencing: Departent of Virology and Human Genome Center, Institute of Medical Science, Theory of the Control of Medical Science, Theory of Theory
                                                                                                                                                                                                                                                                                                           Laboratory of Genome Structure Analysis, Human Genome (Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639, Japan (E-mail:cdnal@ims.u-tokyo.ac.jp, Tel:81-3-5449-5286, Fax:81-3-5449-5416)
                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
Submitted (29-AUG-2000) to the DDBJ/EMBL/GenBank databases. Sumio Sugano, Institute of Medical Science, University of Tokyo, Sugano, Institute of Medical Science, University of Tokyo,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kawabata,A., Hikiji,T., Kobatake,N., Inagaki,H., Ikema,Y., Okamoto,S., Okitani,R., Ota,T., Suzuki,Y., Obayashi,M., Nishi,T., Shibahara,T., Tanaka,T., Nakamura,Y., Isogai,T. and Sugano,S.
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HSA245553 Homo sapiens mRNA
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/clone="CCL09895"
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                                                                                                                                                                     Direct Submission
Submitted (17-AUG-1999) Dobner T.G., Institut fuer Medizinische Mikrobiologie und Hygiene, Universitaet Regensburg, Franz-Josef-Strauss-Allee 11, 93053 Regensburg, GERMANY
                                                                                                                                                                                                                                                      2 (bases 1 to 2878)
Dobner, T.G.
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Dobner, T.G., Fischer, M.
Cloning of a novel zinc
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                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                AP4 gene; AP4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
/gene="AP4"
106. .1776
/gene="AP4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="highly similar to HSA245553 Homo sapiens mRNA for AP4 zinc finger protein" a 974 c 826 g 518 t .
                                                           /cell_line="HeLa"
106. .1776
                                                                                              /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                        1. .2878
                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                            GI:5748564
AP4 protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mRNA PRI
AP4 zinc finger protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 441; DB 3
Pred. No. 5e-62;
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                zinc
                                                                                                                                                                                                                                                                                                         and Groitl, P. finger protein
                                                                                                                                                                                                                                                                                                                                                                                                                                      finger protein
                                                                                                                                                                                                                                                                                                                                                                     Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       37;
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                                                                                                                                                                                                                                                                                                                                                                                        Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                       Homo
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1125

1065

360

1005

300 945 180

825

765 60

885

240

KEYWORDS SOURCE ORGANISM

VERSION ACCESSION DEFINITION FOCUS

RESULT AK025356

REFERENCE AUTHORS

TITLE JOURNAL AUTHORS

COMMENT

FEATURES

source

10

misc\_feature

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REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT
AF201303
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ORIGIN
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                                                                                                                                                                                                                                                                                                  KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                           ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                      DEFINITION
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Best Local Similarity
                                                                 TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       999agcccccagctgccagccggcccccaggagtccgcgggccgagcccaccccggcggta
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CCTCTGAAACCGGCCCAGGAGCCGCCGCCAGGGCCCCGCCAGAGCACCCGCAGGACCCG 1173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CTGTCTCACAGCAAGATTCACAAGCGATCCGAGGGGTCGGCCCAGGCCCCCCGGCCCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGGAGCCCCAGCTGCCAGCCGGCCCCCAGGAGTCCGCGGCCGAGCCCACCCCGGCGGTA
                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
AF201303
The dhfr oribeta-binding protein RIP60 contains 15 zinc fingers: DNA binding and looping by the central three fingers and an associated proline-rich region
                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 2954)

1 (bases, C.R., Montigny, W., Zeltser, L., Dailey, L., Gilbert, J.M. and Deckers, C.R., Montigny, W., Zeltser, L., Dailey, L., Gilbert, J.M. and Deckers, C.R., Montigny, W., Zeltser, L., Dailey, L., Gilbert, J.M. and Deckers, C.R., Montigny, W., Zeltser, L., Dailey, L., Gilbert, J.M. and Deckers, C.R., Montigny, W., Zeltser, L., Dailey, L., Gilbert, J.M. and Deckers, C.R., Montigny, W., Zeltser, L., Dailey, L., Gilbert, J.M. and Deckers, C.R., Montigny, W., Zeltser, L., Dailey, L., Gilbert, J.M. and Deckers, C.R., Montigny, W., Zeltser, L., Dailey, L., Gilbert, J.M. and Deckers, C.R., Montigny, W., Zeltser, L., Dailey, L., Gilbert, J.M. and Deckers, C.R., Montigny, W., Zeltser, L., Dailey, L., Gilbert, J.M. and Deckers, C.R., Montigny, W., Zeltser, L., Dailey, L., Gilbert, J.M. and Deckers, C.R., Montigny, W., Zeltser, L., Dailey, L., Gilbert, J.M. and Deckers, C.R., Montigny, W., Zeltser, L., Dailey, L., Gilbert, J.M. and Deckers, C.R., Montigny, W., Zeltser, L., Dailey, L., Gilbert, J.M. and Deckers, C.R., Montigny, W., Zeltser, L., Dailey, L., Gilbert, J.M. and Deckers, C.R., Montigny, W., Zeltser, L., Dailey, L., Gilbert, J.M. and Deckers, C.R., Montigny, W., Zeltser, L., Dailey, L., Gilbert, L., Dailey, L., Gilbert, J.M. and Deckers, C.R., Montigny, W., Zeltser, L., Dailey, L., Gilbert, L., Dailey, L., Gilbert, M., Mandall, M.
                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                             AF201303.1
                                                                                                                                                                                                                                                                                                                                                                                                                 AF201303
                                                                                               Heintz, N.H.
                                                                                                                                                                                                                                                                    human
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973 c 839 g 538 t
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AVPLKRAQEPPPGAPPEHPQDD I EAPPSLYSCDDCGRSSRLERELRAHGRQHTGGRPF
TCAECGKNFGKKTHLYAHSKYHSGERFFACEBCGRRFSQSSHLAAHRRUHADDRFYC
PDCGKAFRHKPYLAAHRRIHTGEKPYVCPDCGKAFRQKSNLVSHRRIHTGERSYACPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LGFACHLCGQSFRGWVALVLHLRAHSAAKRPIACPKCERRFWRRKQLRAHLQRCHPPA
PAARPFICGNCGRSFAQWDQLVAHKRVHVAEALEEAAAKVLGPRSRGRPAVTAPRPGG
DAVDRPFQCACCGKRFRHKPNLIAHRRVHTGERPHQCPECGKRFTNKPYLTSHRRIHT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /protein_id="CAB53100.1" ·
/db_xref="GI:5748565"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="AP4 protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /codon_start=1
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                                                                                                                                                                                                                                                                                                                             GI:6716713
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dhfr
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oribeta-binding
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 441; DB 7
Pred. No. 5e-62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                protein RIP60 mRNA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
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AUTHORS
TITLE
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ORIGIN
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ggtggagatgccgtcgaccgcccttccagtgtgcctgttgtggcaagcgcttccggcac
                                                                                                                                                                               atcgaagcccccccctcctc 441
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gagtgcgggaagcgctttaccaataagccctatctgacttcgcaccggcgcatccacacc
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Direct Submission
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Gilbert, J.M. and
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This clone was derived from human PAC library RPCI-4, prepared Pieter de Jong and coworkers at the Roswell Park Cancer Institute (http://bacpac.med.buffalo.edu) using the method described by Ioannou et al., Nature Genetics 6:84-9 (1994). The library is
                                                                                                                                                                                                                The sequence of this clone was established as part of a mapping an sequencing collaboration between the NHGRI Chromosome 7 Mapping Project (Eric D. Green, Director), John D. McPherson in the Department of Genetics (Washington University), and the Washington University Genome Sequencing Center. For additional information about the map position of this sequence, see
                                                                                                                                                                                                                                                                                                                                                                                                                                                               This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
Submitted (30-SEP-2000) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108,
On Jun 12, 2000 this sequence version replaced gi:3907529.
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Submitted (12-JUN-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St.
                                                                                                                                                                http://www.nhgri.nih.gov/DIR/GTB/CHR7 mailto:egreen@nhgri.nih.gov , or see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.
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                                                                                                             SOURCE INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                      MAPPING INFORMATION:
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Sulston, J.E. and Waterston, R.
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Web site: http://genome.wustl.edu/gsc
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VECTOR: pCYPAC2
NEIGHBORING SEQUENCE INFORMATION:
The clone sequenced to the right is RP5-820A21, 200 base pair overlap. Actual start of this clone is at base position 1 of RP4-584D14; actual end is at base position 131954 of RP4-584D14.
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                                                                                                                                                                                                                          /rpt_family="MER4-group" 6695. .7007
                                                                                                                                                                                                                                                               /rpt_family-"Alu" 6453. .6690
                                                                                                                                                                                                                                                                                                                                                                                     /rpt_family-"AT_rich" 5679. .5773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /rpt_family="MER4-group" 4872. .5309
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                    7886.
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7180.
                                                            7883.
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/clone="RP4-584D14"
                                         note="match
                                                                             note="match to EST AI144211 (NID:g3666020) qb93g11.x1"
                                                                                                                                                                                                                                                                                                                          'note="match to EST AA482420 (NID:g2210098) zt34f02.r1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="CpG_island (%GC=70.7, o/e=0.90, #CpGs=107)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="similar to
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                                                                                                                     rpt_family="MER4-group"
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                                       to EST W72943 (NID:g1383235) zd54f12.rl"
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GGCGAGAAGCCCTACCCGTGCAAAGAGTGCGGCCGCCGCTTCCGGCACAAACCCAACCTG
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441; Conserv
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8841. .9377
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8835. .9229
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8440. .8968
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8591. .9167
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8459. .8461
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8433. .8746
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="match to EST R72488 (NID:g846520) yj90g06.r1"
7976. .8575
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                                                                                                                                                                                          Score 441; DB 9;
Pred. No. 9.5e-63;
Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (17-NOV-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On May 30, 2000 this sequence version replaced gi:7249370. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Birren,B., Linton,L., Nusbaum,C. and Lander,E. Mus musculus chromosome, clone CT7-315E6
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Sequencing vector: M13; M77815; 44% of reads Sequencing vector: Plasmid; n/7815; 44% of reads Sequencing vector: Plasmid; n/a; %-0.f% of reads 55.555555555556Chemistry: Dye-primer-amersham; 58 Chemistry: Dye-terminator Big Dye; 42% of reads Assembly program: Phrap; version 0.960731 Consensus quality: 192611 bases at least Q40 Consensus quality: 195150 bases at least Q30 Consensus quality: 197810 bases at least Q20
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                                                                                                                                                                                                                                                                                                       Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                       Center clone name: 315_E
                                                                                                                                                                                                                                                                             Center project name: L742
                                                                                                                                                                                                                                                                                                                                                               Web site: http://www-seq.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                        Center: Whitehead Institute/ MIT Center code: WIBR
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NOTE: This is a 'working draft' sequence. It currently consists of 20 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as
                                                                                                                                                                                                                                                                                                                                                                                    130096 163192: contig of 38166 163293 201458: contig of 38166
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Insert size: 199558; sum-of-contigs
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1061 1160: gap of 100 bp
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7380:
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144871: contig of 13922 bp
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15194: contig of 1772 bp in
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2000: contig of 1440 b,
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99150: contig of 24911 bp in length
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24037: contig of 3644 bp in length
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61254: contig of 16283 bp in length
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Best Local Similarity 83.4
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TITLE
                               AUTHORS
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                          Bloecker,H.,
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Pred. No. 3.8e-31;
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                                                                                                                                                                         mRNA PRI 23-MAR-2000 DKFZp762K135 (from clone DKFZp762K135)
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                                 Mewes, H.W., Weil, B. and
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                                                                                                    AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    188 agccctacccgtgcaaagagtgcggccgccttccggcacaaacccaacctgctgtctc 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                128 ggaagegetttaceaataageeetatetgaettegeaceggegeateeaeaceggegaga 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              68 acttgatcgctcaccgcgcgtgcacacggggcgagcggccccaccagtgccccgagtgcg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8 atgccgtcgaccgcccttccagtgtgcctgttgtggcaagcgcttccggcacaagccca
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACCGCAAGAGCCACATCCGGGACGGCGCCTTCTGCTGTGCCATCTGTGGCCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      199;
                                                                                                                                                                                                                                                                                                                                  Homo sapiens chromosome 7 clone RP11-143I21, SEQUENCE, 6 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de Further
information about the clone and the sequencing project is available
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de; sequenced by GBF (National Research Centre for Biotechnology Ltd. Braunschweig/Germany) within the cDNA sequencing consortium of the
                                     Direct Submission
Submitted (14-JUN-2000) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St.
                                                                                                                                                                                                                                                                                                      HTG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      at http://www.mips.biochem.mpg.de/proj/cDNA/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Please contact the RZPD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         German Genome Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Martinsried,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (15-MAR-2000) MIPS, Am Klopferspitz 18a,
                                                                                                2 (bases 1 to 162570)
Waterston, R.H.
                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This clone (DKF2p762K135) is available at the RZPD in Berlin
                                                                                                                                                          The sequence of Homo sapiens clone
                                                                                                                                                                                Waterston, R.H.
                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                    AC073314.2 GI:8954230
                                                                                                                                       Unpublished
  63108,
Jul 7,
                                                                                                                                                                                                   (bases
                                                                                                                                                                                                                                                                                                  HTGS_PHASE1; HTGS_DRAFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone="DKFZp762K135"
/clone_lib="762 (synonym: hmel2). Vector pSport1; host
DH10B; sites NotI + SalI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /tissue_type="melanoma (MeWo cell line)"
246 c 252 g 144 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /dev_stage="adult"
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                        USA
                                                                                                                                                                                                 1 to 162570)
2000 this sequence version replaced gi:8516162.
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Pred. No. 4.9e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                   Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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BASE COUNT
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                                     11 ccgtcgaccgccccttccagtgtgcctgttgtggcaagcgcttccggcacaagccccaact 70
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Quality coverage: 7.94 in Q20 bases; agarose-fp Quality coverage: 8.07 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Insert size: 164000; agarose-fp Insert size: 162070; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequencing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequencing vector: M13; 66%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Center project name: H_NH014312:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Web site:http://genome.wustl.edu/gsc/index.shtml
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Center code: WUGSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Center: Washington University Genome
                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NOTE: This is a 'working draft' sequence. It currently consists of 6 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                              44044
                                                                                                                                          Conservative
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36049 c 36050
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96970. .162570
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="assembly_name:Contig16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'note="assembly_name:Contig14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       note="assembly_name:Contig12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone="RP11-143I21"
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44491: contig of 31734 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Summary Statistics
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1362:
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gap of unknown length
contig of 3228 bp in length
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                                                                                                                                          Score 134.6; DB 5
Pred. No. 9.2e-14;
0; Mismatches 164
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least Q30
least Q20
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                                                                                                                                                                                Direct Submission
Submitted (19-SEP-1998) Department of Genetics,
University, 4444 Forest Park Avenue, St. Louis,
4 (bases 1 to 128361)
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Direct Submission
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              Contact: sapiens@watson.wustl.edu
Center project name: H_DJ0751H13
                                             Web site:
                                                             Center code: WUGSC
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clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted: all regions were double stranded or sequenced with an alternate chemistry; an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was sequence from more than one subclone; confirmed by restriction digest.

## MAPPING INFORMATION:

The sequence of this clone was established as part of a mapping and sequencing collaboration between the NHGRI Chromosome 7 Mapping Project (Eric D. Green, Director), John D. McPherson in the Department of Genetics (Washington University), and the Washington University Genome Sequencing Center. For additional information about the map position of this sequence, see http://www.nhgri.nih.gov/DIR/GTB/CHR7, send mailto:egreen@nhgri.nih.gov/DIR/GTB/CHR7). send mailto:egreen@nhgri.nih.gov or see http://genome.wustl.edu/gsc actual The clone sequenced to the left is RP4-811N16, start of this clone is at base position 1 of RP4-751H13; end is at 128361 of RP4-751H13.

Location/qualifiers .128361 200 bp overlap

FEATURES misc\_feature misc\_teature misc\_feature misc\_feature misc\_feature repeat\_region repeat\_region source repeat\_region /rpt\_ 11605 /rpt\_family="L2" 9100. .9426 10297 complement(9947 /rpt\_family="Alu" 7787. .7870 9947. /map="7q35-qter" /clone="RP4-751H13" /organism="Homo sapiens" /db\_xref="taxon:9606" /rpt\_family="Retroviral"
12617. .12755 note="match 10066. note="match note="match 'note="match to EST 'note="match to EST rpt\_family="L2" rpt\_family="Retroviral" 'rpt\_family="Retroviral" 'rpt\_family="Alu" clone\_lib="unknown" /chromosome="7 rpt\_family="Malk" rpt\_family="Alu" rpt\_family="MER1\_type?" \_family="MIR" \_family="L1" \_family="Alu" family="L1" family="MaLR" .8145 .4287 .10370 .10086 .8311 . 6243 .10734 .10388 .12615 3246 2885 to EST to EST to EST AA828832 .10370) ST AA828832 (NID:g2901931) AA080867 AA857387 (NID:g2945689) od83h10.s1" AA084720 (NID:g2901931) (NID:g1623560) (NID:g1626811) od80c03.s1" od80c03.s1" zn06f02. zn06f02.r1"

NOTICE:

This sequence may not represent the entire insert of this

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/note="match to EST AA771702 (NID:g2823485) a132a10.s1"
complement(20059. .20239)
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/note="match to EST AA939299 (NID:g3099212) o178g08.
19479. .19656
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13314. .1:
                                                                                                                             20298. .20740
/note="similar to Mus musculus
mh85f12.r1"
                                                                                                                                                                                                                    /note="match to EST AA923119 (NID:g3070428) ok91e12.s1" complement(20097. .20319) /gene="MUSCS:H_UO0751H13.3" /note="match to EST AA885789 (NID:g3000897) oj35a06.s1"
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H_DJ0751H13.3"
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PFSCPQCGKSFSRKTHLVRHQLIHGEAAHAAPDAALAAPAWSAPPEVAPPPLFF"
                                                                                                                                                                                                                                                                                                                                                                                                                                    THKQHLVRHQRVHQTAGPARPSPDSSASPHSTAPSPTPSFPGPKPFACSDCGLSFGWK
KNLATHQCLHRSEGRPFGCDECALGATVDAPAAKPLASAPGGPGCGPGSDPVVPQRAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /translation="MIRKVKVEDEDQEAEEEVEWPQHLSLLPSPFPAPDLGHLAAAYK
LEPGAPGALSGLALSGWGPMPEKPYGCGECERRFRDQLTLRLHQRLHRGEGPCACPDC
GRSFTQRAHMLLHQRSHRGERPFPCSECDKRFSKKAHLTRHLRTHTGERPYPCAECGK
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complement(19861. .20173)
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12891. .13196
       /rpt_family="MIR"
22848. .23146
                                          /note="match to EST 22351. .22486
                                                                                                                                                                                                                                                                                                                                                                                                                     SGERSFFCPDCGRGFSHGQHLARHPRVHTGERPFACTQCDRRFGSRPNLVAHSRAHSG
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/db_xref="GI:3638956"
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                                                                           /note="match to EST AA044857
20819. .21219
                                                                                                                                                                                   note="match to EST AA894411
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                                                                                            (NID:g1523196) zf54d12.r1"
                                                                                                                                                                                   (NID: 93030812)
                                                           (NID:g2805691) zg44d02.sl"
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Best Local Similarity Matches 177; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CCTACCAGTGCGCACAGTGCGCACGCAGCTTCACGCACAAGCAGCACTTGGTGCGGCACC 20842
                                                                                                                                                                                                                                                                                                                                210923 bp DNA HTG 15-JUL-2000
Homo sapiens chromosome 7 clone RP11-428D5, WORKING DRAFT SEQUENCE, 10 unordered pieces.
ACC13273
                  Direct Submission
Submitted (05-NOV-1999) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St.
MO 63108, USA On Jul 15, 2000 this sequence version replaced gi:8990985
                                                                                                                                                          The sequence of Homo sapiens clone
                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 210923)
                                                                                                  Waterston, R.H.
                                                                                                                                      Unpublished
                                                                                                                                                                                Waterston, R.H.
                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                              HTG; HTGS_PHASE1; HTGS_DRAFT.
                                                                                                                                                                                                                                                                                                                    AC013273.5 GI:9211421
                                                                                                                    (bases 1 to 210923)
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26933. .29260
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23679. .23794
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--- Genome Center ----

Sequencing Center

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BASE COUNT
ORIGIN
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 Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Quality coverage: 4.85 in Q20 bases; agarose-fp Quality coverage: 4.93 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Insert size: 203000; agarose-fp
Insert size: 210023; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chemistry: Dye-terminator Big Dye; 26% of Assembly program: Phrap; version 0.990319
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  as soon as it
be preserved.
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11908
                                                                                /note="assembly_name:Contig16"
150744. .210923
/note="assembly_name:Contig17"
51422 c 51731 g 52663 t
                                                                                                                                                                                    vector_side:left"
63763. .104507
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                                                                                                                                                    /note="assembly_name:Contig15"
104608. .150643
                                                                                                                                                                                                                                    note="assembly_name:Contig14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                      note="assembly_name:Contig13"
                                                                                                                                                                                                                                                                                                                                      note="assembly_name:Contig12"
                                                                                                                                                                                                                                                                                                                                                                        note="assembly_name:Contig11"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         note="assembly_name:Contig8"
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g of 7090 bp in le
renown length
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of 8734
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 2094)
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Gene 106 (2), 221-227 (1991)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Denny, P. and Ashworth, A.
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                                                                                                                                                                                                                                                                                                 /gene="zfp-29"
104. 1948
/gene="zfp-29"
                                 CGKSFSQSSSLIAHQGTHTGEKPYECL#CGESFSWSSNLIKHQRTHTGEKPYRCGDCG
KGFSQRSQLVVHQRTHTGEKPYKCL#CGKSFSRGSILVMHQRAHLGDKPYRCPECGKG
                                                                      SCPECGKSFGNRSSLNTHQGIHTGEKPYACKECGESFSYNSNLIÄHRRTHLVEKPYKCGL
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/db_xref="GI:55471"
/db_xref="SWISS-PROT:Q07230"
                   FSWNSVLIIHQRIHTGEKPYRCPECGKGFSNSSNFITHQRTHLKEKLY"
                                                                                                                                                                                                                                                                                                                                                                              /dev_stage="adult male"
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                                                                                                                                                                                                                                                                                    /codon_start=]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           strain="ssp.
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98290545
                                                                                                                                                              Nagase,T., Ishikawa,K., Miyajima,N., Tanaka,A., Kotani,H., Nomurz,N. and Ohara,O.
Prediction of the coding sequences of unidentified human genes. IX.
The complete sequences of 100 new cDNA clones from brain which can code for large proteins in vitro
DNA Res. 5 (1), 31-39 (1998)
                                                                                                                                                                                                                                                                                 Submitted (13-FBB-1998) to the DDBJ/EMBL/GenBank databases. Osamu Ohara, Kazusa DNA Research Institute, DNA Technology; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:cdnainfo@kazusa.or.jp, Tel:+81-438-52-3913, Fax:+81-438-52-3914)
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/note="zinc fingers"
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/clone="HH1334"
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 /tissue_type="brain"
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                               /clone_lib="pBluescriptII
/sex="male"
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DKPYTCPECGKGFSKTSHLTKHQRTHTGERPYKCLVCGKGFSDRSNFSTHQRVHTGEK
PYPCPECGKRESQSSSLVIHRRTHSGERPYACTQCGKRFNNSSHFSAHRRTHTGEKPY
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/codon_start=2
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TITLE JOURNAL REFERENCE AUTHORS SOURCE ORGANISM VERSION KEYWORDS RESULT 12 AC020663/c REFERENCE DEFINITION ACCESSION Locus AUTHORS 2 (bases 1 to 154218) Ricke, D.O. Han, C. and Deaven, L. Sequencing of Human Chromosome Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eute Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Home 1 (Dases I to 154218) Bruce, D., Mundt, M., Doggett, N., Munk, C., Saunders, E., Rol Jones, M., Buckingham, J., Chasteen, L., Thompson, S., Goodwi Bryant, J., Tesmer, J., Meincke, L., Longmire, J., White, S., Campbell, C., Fawcett, J., Maltble, M., Bussod, M., Sutherlar Homo sapiens Homo sapiens AC020663.1 AC02066 Unpublished AC020663 154218 GI:6682593 54218 bp chromosome DNA 16 PRI clone RPCI-11\_127I20, complete 08-JAN-2000 Goodwin, L., Euteleostomi; Robinson, D., sequence

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1	1264313073 /rpt_family="Alu"	/rpt_family="Alu"	/rpt_family="Alu" 1228212576	/FPC_1dm11Y="M5K42" 11803. 12101	1158011780 	complement(1080110977)		/rpt familv="Alu"	/rpt_family="Alu"	-	/rpt_family="Alu" 9515_ 9812	/rpt_family="Alu" 93949682	/rpt_tamily="Alu" 88089139 -	79318385		complement(68486983) /note="GRAIL 2 excellent exon, frame 1"	57496045 /rnt family="all:"	/rpt_family="Alu"	/rpt_fanily="Alu"		/rpt_family="Alu" complement(38594163)	/rpt_tamily="Alu" complement(35713890)	31873504	24982795	21762372 /rpt family="1.1"	18712190 /rpt_family="Alu"	15951862 /rpt_family="Alu"	1414 .1712 /rpt_family="Alu"	/rpt_family="Alu"	Complement(41330) /rpt_family="Alu" Fre	/close="RPCI-1127120"	/db_xref="taxon:9606"	1154218 /organism="Homo sapiens"	m 6/343, USA Location/Qualifiers	08-JAN-2000) Center for H itute, Los Alamos Nationa	Han,C. and Deaven,L.	esmer,J., meincke,L., Lo Fawcett,J., Maltbie,M.,	ckingham, J., Chasteen, L., Thompson, S., Goodwi	to 154218)	le Sequence Analysis and Annotation with the Sequence n Analysis (SCAN) System	_
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	<pre>/note="GRAIL 2 excellent exon, frame 0" complement(3792037961)</pre>			33495 family="Alu"	/rpt_family="Alu"	/rpt_family="LTR37B" 34576 34556	/rpt_family="Alu" complement(3420234278)	/rpt_family="Alu" 3364934040	32507. 32839	complement(3230232492)	3205932124 /rnt }amilv="Alu"	3130031655 /rpt_family="Alu"	3059730772 /note="GRAIL 2 excellent exon, frame 2"	/rpt_family="Alu"	/rpt_family="Alu"	/rpt_family="Alu" /rpt_family="Alu" complement(26044 26355)	/rpt_family="L1" 25914 25981	/rpt_ramily="Alu" 2560525862	25205	complement(2404624341) /rpt familv="Alu"		<pre>complement(2278922948) /note="GRAIL 2 excellent exon, frame 1"</pre>			<pre>/rpt_family="MER20" complement/20808 21104)</pre>	<pre>/note="GRAIL 2 excellent exon, frame 1" 2023920397</pre>	C		complement(1851818917)	complement(1842018718)	16559. 16831	complement(1619216347)  /rot family="Ali"	<pre>complement(1608316185) /rpt family="L1"</pre>		1506115366 /rpt_family="Alu"	<pre>complement(1440114696) /rpt_family="Alu"</pre>		13/6114148 /rpt_family="Alu"	1342013/25 /rpt_family="Alu"	1292313237 /rpt_family="Alu"	

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LOCUS HSJ599G15 138278 bp
DEFINITION Homo sapiens chromosome
                                               HSJ599G15/c
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Best Local Similarity
Matches 242; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                             45444 AGCCCTACCCGTGCCCCGAGTGTGGGAAGCGCTTCAGCCAGAGCTCCAGCCTGGTCATCC
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                                                                                                                                                                                                                                   45329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       45504 GGAAGGGCTTTAGCGACCGCTCCAACTTCAGCACGCACCAGAGGGTGCACACAGAGGCGAGA 45445
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                                                                                                                                                                368 aaccggcccaggagccgccgccaggggccccgccagagcacc 409
                                                                                                                                                                                                                                                                                                                                                                     248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      68 acttgatcgctcaccgcgcgtgcacacgggcgagcggcccaaccagtgccccgagtgcg 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8 atgccgtcgaccgcccttccagtgtgcctgttgtggcaagcgcttcccggcacaagccca 67
                                                                                                                                                                                                                                                                                                                                                    acagcaagattcacaagcgatccgaggggtcggcccaggccgccccgggcccggggagcc 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                     agccctacccgtgcaaagagtgcggccgccgcttccggcacaaacccaaacctgctgtctc 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99aagegetttaeceataageeetatetgaettegeaceggegeateeacaceggegaga 187
                                                                                                                                         CACCTGCCC -- GGCCTGTGGCCGGGGCTTCCGCCGGGGCACC 45230
                                                                                                                                                                                                                                CTTCAACAACAGCTCGCACTTCAGCGCCCACCGCCGGACGCACAGGTGAGAAGCCCTA
                                                                                                                                                                                                                                                        cccagctgccagccggcccccaggagtccgcgggccgagcccaccccggcggtacctctga 367
                                                                                                                                                                                                                                                                                                                      ACCGCAGGACACAC-----AGCGGGGAGCGGCCCTATGCCTGCACCCAGTGCGGGAAGCG
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/rpt_family="Alu"
complement(43274.
/rpt_family="Alu"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement(46300.
/note="GRAIL 2 exc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /rpt_family="MER3"
complement(40939.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              _family="Alu"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 123.2; DB 10; Lengtl
Pred. No. 6.3e-12;
0; Mismatches 153; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 excellent exon,
DNA HTG 06-OCT-2000 1 clone RP4-599G15 map p12-13.2, ***
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  misc_feature
                                                                  misc_feature
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                                                                                                                                                                                                                                                                                                source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chemistry: Dye-terminator ET-amersham; 0% of reads Chemistry: Dye-terminator ABI; 1% of reads
Chemistry: Dye-terminator Big Dye; 94% of reads
Chemistry: Dye-primer-amersham; 2% of reads
Chemistry: Dye-primer Big Dye; 1% of reads
Consensus quality: 136114 bases at least 040
Consensus quality: 137176 bases at least 020
Consensus quality: 137544 bases at least 020
Insert size: 137778; sum-of-contigs
Insert size: 136114; 2.3% error; agarose-fp
Quality coverage: 6.30x in 020 bases; sum-of-contigs Quality
Coverage: 8.38x in 020 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequencing vector: M13; M77815; 25% of reads Sequencing vector: plasmid; L08752; 74% of reads
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
------ Project Information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (04-OCT-2000) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 138278)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     * NOTE: This is a 'working draft' sequence. It currently consists of 6 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Center project name: dJ599G15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Assembly program: XGAP4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Center code:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Donnelly,S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               be preserved.
                                                                                                                                                                                                                                                                                                            8020: contig of 8020 bp in length
8021 8120: gap of 100 bp
8121 15996: contig of 7876 bp in length
15997 16096: gap of 100 bp
16097 19055: contig of 2959 bp in length
19056 19155: gap of 100 bp
19156 22087: contig of 2932 bp in length
22088 22187: gap of 100 bp
22188 29998: contig of 7811 bp in length
22999 30098: gap of 100 bp
138278: contig of 108180 bp in length
100cation/Qualifiers
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                                                                  /note="assembly_fragment:01125
fragment_chain:1"
8121. .15996
/note="assembly_fragment:02016
fragment_chain:1"
16097. .19055
                                                                                                                                                                                                                                                                                                1. .138278
                                                                                                                                                                                                                                               /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                            clone_
                                                                                                                                                                               /clone="RP4-599G15"
                                                                                                                                                                                                      map="p12-13.
                                                                                                                                                                                                                            'chromosome="
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 94213 CTTCAGCTGGCGCGCCGACCTGCTCAAGCACCGGCGCCTGCACACGGGCGAGAAGCCCTA
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                                                                        Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M., Baker, J., Baldwin, J., Barna, N., Beckerly, R., Benn, J., Brown, A., Castle, A., Cerny, J., Colangelo, M., Collins, S., Collymore, A., Cooke, P., Dexrellano, K., Depayre, E., Devon, K., Dewar, K., Donelan, L., Doyle, M., Ferreira, P., Fitzhugh, W., Forrest, C., Funke, R., Gage, D., Galagan, J., Gardyna, S., Gilbert, D., Grant, G., Feuke, R., Gage, D., Galagan, J., Gardyna, S., Gilbert, D., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J.C., Jones, C., Kann, L., Karatas, A., Lehoczky, J., Lieu, C., Locke, K., McClaughlin, J., Marquis, N., McEwan, P., McGurk, A., McKernan, K., McLaughlin, J., Meldrim, J., Molla, M., Morris, W., Morrow, J., Mychalecky, J., Meddrim, J., Molla, M., Morris, W., Morrow, J., Mychalecky, J., Naylor, J., Niloff, M., O'Connor, T., O'Donnell, P., Pavlin, B., Peterson, K., Pollara, V., Riley, R., Roberts, D., Roy, A., Severy, P., Stange-Thomann, N., Stojanovic, N., Stone, C., Subramanian, A., Tesfaye, S., Torruella-Miller, I., Vassiliev, H., Vo, A., Wagner, A., Wheeler, J., W. X., Wwan, D., Ye, W. J. and Zodv M.
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                          Submitted
                                              Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus chromosome,
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                                                             Wheeler, J., Wu, X., Wyman, D., Ye, W.J. and Zody, M.
                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished
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(Dases I tinton,L., Nusbaum,C. and Lander,E. rren,B., Linton,C., Nusbaum,C. and Lander,E.
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clone_end:T7
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19156. .22087
(08-MAY-1999) Whitehead Institute/MIT Center for Genome 320 Charles Street, Cambridge, MA 02141, USA
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- clone CT7-345D4,
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                                                                                                                                                                                                                                                                                                                                                                                                                                         cctacccgtgcaaagagtgcggccgcgcttccggcacaaacccaacctgctgtctcaca 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     agcgctttaccaataagccctatctgacttcgcaccggcgcatccacacccggcgagaagc 190
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                                                                                                                                                                                                                                                            CAGGTGCAAG 23438
                                                                                                                                                                                                                                                                                                   cagctgccag 319
                                                                                                                                                                                                                                                                                                                                       AGCGCTTCACGCAGAAGCACCACCTGCTGGAGCATCAGCGTGCGCACACAGGCGAGCGGC 23308
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                      Homo sapiens
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This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

1 29802: contig of 29802 bp in length.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NOTE: This is a 'working draft' sequence. It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces \frac{1}{2}
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: sequence_submissions@genome.wi.mit.edu
----- project Information
Center project name: L738
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Web site: http://www-seq.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Center code: WIBR
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/db_xref="taxon:10090"
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Pred. No. 6.5e-11;
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CGGCCAAGGTGCTGGCGGCTAGCGTCCGGCGGGCCAAGGGGCCCGA
                  cggcccaggagccgccgccagggccccgccagagcacccgcagga 416
                                                                                 agctgccagccggcccccaggagtccgcggccgagcccaccccggcggtacctctgaaac 370
                                                                                                               AGCGCTTCAGCTGGAGCTCCAACCTCATGCAGCACCAGCGCATCCACACGGGCGAGAAGC
                                                                                                                                                                                                                                                                                         TGGTGCAGCACCGGCGCATCCACACGGGCGAGAAGCCCTACGCCTGCTTGGAGTGCGGCA 394
                                                                                                                                                                                                                                                                                                                                                 CCGGCGAGCGGCCCAACGCCTGCGCCGACTGCGGCAAGACCTTCTCGCAGAGCTCGCACC 334
                                                       AGCCCAAGAGCCTCGCGCGTCACCTGCGGCTGCACCCGGAGCTGTCGGGGGCCTGGCGTGG 634
                                                                                                                                                                                                                                                                                                                                                                                                          226;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
Submitted (21-APR-1997) Molecular Biology of the Cell II, German
Cancer Research Center, Im Neuenheimer Feld 280, Heidelberg, B.-W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Jansa, P. and Grummt, I.
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                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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Interacting Peptide 20"
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/cell_type="fibroblasts"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/db_xref="taxon:9606"
/cell_line="WI-38"
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55.7%;
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Pred. No. 2.9e-10;
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Search completed: February 22, Job time: 15062 sec

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